



PT to induce specific T cell tolerance, esp. for treatment of  
 PT rheumatoid arthritis, also useful in producing arthritic animal  
 PT models  
 PA Claim 1: Page 28; 37pp; English.  
 XX The present peptide, derived from the human cartilage glycoprotein  
 XX 39 (HC gp-39) autoantigen, can be used to induce T-cell tolerance  
 XX to cartilage, or HC gp-39 in a patient with T-cell mediated cartilage  
 XX destruction, esp. rheumatoid arthritis (RA). It may also be used to  
 XX induce T-cell tolerance to cartilage, or HC gp-39 in a patient with  
 XX the presence of activated T-cells autoreactive with HC gp-39, i.e. to  
 XX identify patients suitable for tolerin treatment, 1-100 microg/kg  
 XX by injection, or 10-50 microg/kg to produce a disease model. The  
 XX peptide has a specific tolerizing effect on autoreactive T-cells,  
 XX therefore should have few side effects. In an assay to determine  
 XX the peptide's binding to HA-DR moieties, specifically DRB2\*04 (known  
 XX to be a major HLA-DR allele in RA), the peptide gave a DOR blot (C501 microtiter) value of 0.04 compared  
 XX to 0.52 for the control peptide 1HA(107-319).  
 XX Sequence 9 AA:

Query Match 100.0% Score 44; DS 17; Length 9;  
 Mismatches 0; Conservativity 0; Mismatches 0; Gaps 0;

QY 1 F08SFTLAS 9  
 DE 1 F08SFTLAS 9

RESULT 2  
 10 AAV69226 standard; peptide, 9 AA.  
 XX AAV69226;  
 XX AAV69226 standard; peptide, 9 AA.

XX 30-MAY-2000 (first entry)  
 XX Peptide (fragment of human cartilage gp-39 (HC gp-39) protein.  
 XX Human cartilage gp-39 protein; HC gp-39 protein; T-cell activator;  
 XX antigen-specific T-cell tolerance; autoimmune disorder;  
 XX inflammatory disease; rheumatoid arthritis;  
 XX autoimmune inflammatory disease; autoantigen.  
 XX Bone saplens.  
 XX NC020004917-A2.  
 XX 03-FEB-2000.  
 XX 15-JUL-1999; 95NC-EP05311.  
 XX 23-JUL-1996; 95EP-0202473.  
 XX (ALU) AKZO NOBEL NV.  
 XX Miltentburg MM, Roets AMH;  
 XX WPI: 2000-162337/15.  
 XX Use of cartilage protein or peptides for treating inflammatory diseases  
 XX especially rheumatoid arthritis  
 XX Claim 2: Page 17; 2pp; English.  
 XX AAV69226-33 represent fragments of the human cartilage gp-39 (HC gp-39)  
 XX protein. The peptides are T-cell activators. The peptides are used for

CC preventing inflammatory diseases, by modulating lymphocyte reactivity  
 CC to antigens other than HC gp-39, present in the same tissue of  
 CC HC gp-39. By the induction of antigen specific T-cell tolerance,  
 CC HC gp-39 protein, or fragments thereof, can be used to suppress the  
 CC HC gp-39 peptides are useful for preventing inflammatory diseases,  
 CC especially rheumatoid arthritis. The fragments may also be used for  
 CC treating autoimmune inflammatory diseases. The HC gp-39 peptides are  
 CC autoantigens associated with the condition are unknown.  
 XX Sequence 9 AA:

Query Match 100.0% Score 44; DS 21; Length 9;  
 Mismatches 0; Conservativity 0; Mismatches 0; Gaps 0;

QY 1 F08SFTLAS 9  
 DE 1 F08SFTLAS 9

RESULT 3  
 10 AAV95073 standard; peptide, 13 AA.  
 XX AAV95073 standard; peptide, 13 AA.

XX AAV95073;  
 XX 17-DEC-1996 (first entry)  
 XX Peptide contg. HC gp-39 autoantigen derived peptide (1).  
 XX Human cartilage glycoprotein 39; HC gp-39; autoantigen;  
 XX antigen-specific T-cell tolerance; autoimmune disorder;  
 XX inflammatory disease; rheumatoid arthritis; disease model; diagnosis.  
 XX Bone saplens.  
 XX NC020004917-A2.  
 XX 03-FEB-2000.  
 XX 15-JUL-1999; 95NC-EP05311.  
 XX 23-JUL-1996; 95EP-0202473.  
 XX (ALU) AKZO NOBEL NV.  
 XX Miltentburg MM, Roets AMH;  
 XX WPI: 2000-162337/15.  
 XX Use of cartilage protein or peptides for treating inflammatory diseases  
 XX especially rheumatoid arthritis  
 XX Claim 2: Page 17; 2pp; English.  
 XX AAV95073-33 represent fragments of the human cartilage gp-39 (HC gp-39)  
 XX protein. The peptides are T-cell activators. The peptides are used for

XX 30-MAY-2000 (first entry)  
 XX Peptide (fragment of human cartilage gp-39 (HC gp-39) protein.  
 XX Human cartilage glycoprotein 39; HC gp-39; autoantigen;  
 XX antigen-specific T-cell tolerance; autoimmune disorder;  
 XX inflammatory disease; rheumatoid arthritis; disease model; diagnosis.  
 XX Bone saplens.  
 XX NC020004917-A2.  
 XX 03-FEB-2000.  
 XX 15-JUL-1999; 95NC-EP05311.  
 XX 23-JUL-1996; 95EP-0202473.  
 XX (ALU) AKZO NOBEL NV.  
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XX 30-MAY-2000 (first entry)  
 XX Peptide (fragment of human cartilage gp-39 (HC gp-39) protein.  
 XX Human cartilage glycoprotein 39; HC gp-39; autoantigen;  
 XX antigen-specific T-cell tolerance; autoimmune disorder;  
 XX inflammatory disease; rheumatoid arthritis; disease model; diagnosis.  
 XX Bone saplens.  
 XX NC020004917-A2.  
 XX 03-FEB-2000.  
 XX 15-JUL-1999; 95NC-EP05311.  
 XX 23-JUL-1996; 95EP-0202473.  
 XX (ALU) AKZO NOBEL NV.  
 XX Miltentburg MM, Roets AMH;  
 XX WPI: 2000-162337/15.  
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 XX Claim 2: Page 17; 2pp; English.  
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 XX protein. The peptides are T-cell activators. The peptides are used for

XX 30-MAY-2000 (first entry)  
 XX Peptide (fragment of human cartilage gp-39 (HC gp-39) protein.  
 XX Human cartilage glycoprotein 39; HC gp-39; autoantigen;  
 XX antigen-specific T-cell tolerance; autoimmune disorder;  
 XX inflammatory disease; rheumatoid arthritis; disease model; diagnosis.  
 XX Bone saplens.  
 XX NC020004917-A2.  
 XX 03-FEB-2000.  
 XX 15-JUL-1999; 95NC-EP05311.  
 XX 23-JUL-1996; 95EP-0202473.  
 XX (ALU) AKZO NOBEL NV.  
 XX Miltentburg MM, Roets AMH;  
 XX WPI: 2000-162337/15.  
 XX Use of cartilage protein or peptides for treating inflammatory diseases  
 XX especially rheumatoid arthritis  
 XX Claim 2: Page 17; 2pp; English.  
 XX AAV95073-33 represent fragments of the human cartilage gp-39 (HC gp-39)  
 XX protein. The peptides are T-cell activators. The peptides are used for

CC Peptide has a specific tolerizing effect on autoreactive T-cells,  
CC but leaves cellular immune system intact, and  
CC therefore should have low side effects.

XX Sequence 13 AA:

Query Match: 100.0%; Score 44; DB 21; Length 13;

XX Identical similarity: 100.0%; Positives: 0.074; Gaps: 0;

XX Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0;

Oy 1 F0RSTIAS 9

Db 1 F0RSTIAS 9

1 F0RSTIAS 9

3 F0RSTIAS 11

RESULT 4

AMF9230

1D AMF9230 standard; peptide: 13 AA.

XX Query Match: 100.0%; Score 44; DB 21; Length 13;

XX Identical similarity: 100.0%; Positives: 0.074; Gaps: 0;

XX Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0;

Oy 1 F0RSTIAS 9

Db 1 F0RSTIAS 9

1 F0RSTIAS 9

3 F0RSTIAS 11

RESULT 5

AMF9230

1D AMF9230 standard; peptide: 13 AA.

XX Query Match: 100.0%; Score 44; DB 21; Length 13;

XX Identical similarity: 100.0%; Positives: 0.074; Gaps: 0;

XX Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0;

Oy 1 F0RSTIAS 9

Db 1 F0RSTIAS 9

1 F0RSTIAS 9

3 F0RSTIAS 11

RESULT 6

AMF9224

XX AMF9224 standard; peptide: 13 AA.

XX Query Match: 100.0%; Score 44; DB 21; Length 13;

XX Identical similarity: 100.0%; Positives: 0.074; Gaps: 0;

XX Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0;

Oy 1 F0RSTIAS 9

Db 1 F0RSTIAS 9

1 F0RSTIAS 9

3 F0RSTIAS 11

RESULT 7

AMF9224

XX AMF9224 standard; peptide: 13 AA.

XX Query Match: 100.0%; Score 44; DB 21; Length 13;

XX Identical similarity: 100.0%; Positives: 0.074; Gaps: 0;

XX Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0;

Oy 1 F0RSTIAS 9

Db 1 F0RSTIAS 9

1 F0RSTIAS 9

3 F0RSTIAS 11

RESULT 8

AMF9224

XX AMF9224 standard; peptide: 13 AA.

XX Query Match: 100.0%; Score 44; DB 21; Length 13;

XX Identical similarity: 100.0%; Positives: 0.074; Gaps: 0;

XX Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0;

Oy 1 F0RSTIAS 9

Db 1 F0RSTIAS 9

1 F0RSTIAS 9

3 F0RSTIAS 11

RESULT 9

AMF9230

1D AMF9230 standard; peptide: 13 AA.

XX Query Match: 100.0%; Score 44; DB 21; Length 13;

XX Identical similarity: 100.0%; Positives: 0.074; Gaps: 0;

XX Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0;

Oy 1 F0RSTIAS 9

Db 1 F0RSTIAS 9

1 F0RSTIAS 9

XX AMF9220;

XX AMF9220;

XX AMF9220;

XX AMF9220;

XX AMF9220;

XX AMF9220;

XX AMF9220;

XX AMF9220;

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XX AMF9220;

XX AMF9220;

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XX AMF9220;

XX AMF9220;

XX AMF9220;

XX W0200214870-A1.  
 XX 21-FEB-2002.  
 XX 08-AUG-2001: 2001MO-E09136.  
 XX 14-AUG-2002: 2002EP-020284.  
 XX (AKU) AKZO NOBEL NV.  
 XX Steenbakkers PCA.  
 XX WPI: 2002-266214/31.  
 XX  
 XX Method for diagnosing an autoimmune disease activity by detecting the  
 XX (MHC) peptide complex in a patient using antibodies specific against  
 XX MHC-peptide complexes.  
 XX  
 XX Disclosure: Page 43; 4pp: English.  
 XX  
 XX The patent discloses a method for diagnosing an autoimmune disease  
 XX activity. The method involves detecting the presence of an autoimmune  
 XX specific major histocompatibility complex (MHC) peptide complex in a  
 XX patient's blood. The method involves using antibodies specific against  
 XX antigen binding domains that specifically bind to MHC-peptide  
 XX peptide. The method and antibodies are useful for diagnosing auto-  
 XX immune diseases of purifying autoimmune specific MHC-peptide complexes.  
 XX They are also useful for the treatment of autoimmune disorders such as insulin-  
 XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,  
 XX rheumatoid arthritis, and other autoimmune diseases.  
 XX cartilage glycoprotein (HC 3P-19 peptide (residues 259-271)). This  
 XX peptide is used in the exemplification of the invention.  
 XX  
 XX Sequence 13 AA:  
 XX  
 XX Query Match 100.0%; Score 44; DB 33; Length 33;  
 XX Best Local Similarity 100.0%; Pred. No. 0.04;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 07 1 FOREPTLAS 5  
 XX 3 FOREPTLAS 11  
 XX  
 XX RESULT 7  
 XX W0200214870-A1.  
 XX 10-AMN1595 standard: protein: 15 AA.  
 XX  
 XX AKMS1598:  
 XX 27-OCT-1998 (first entry)  
 XX Human Cartilage 3p-39 epitope (41).  
 XX  
 XX Human Cartilage 3p-39, zonalonol antibody: cell surface antigen;  
 XX rheumatoid arthritis; T-cell receptor.  
 XX  
 XX Homo sapiens.  
 XX PF856520-A1.  
 XX 05-AUG-1998.  
 XX 02-DEC-1997: 97EP-003769.  
 XX 27-JUN-1997: 97EP-030127.  
 XX 06-DEC-1996: 96EP-020346.  
 XX  
 XX (AKU) AKZO NOBEL NV.  
 XX

XX Steenbakkers PCA.  
 XX WPI: 1998-400866/35.  
 XX  
 XX Preparation of monoclonal antibodies against cell surface antigens  
 XX used as diagnostic agents and to treat rheumatoid arthritis  
 XX by preparing hybridomas and cloning B cells  
 XX and then selecting and cloning hybridomas.  
 XX  
 XX Samples: Page 13; 2pp: English.  
 XX  
 XX The human cartilage 3p-39 peptides AMN1597-AM1599 were used in the  
 XX preparation of monoclonal antibodies against cell surface antigens.  
 XX The antibody can be used for treatment of rheumatoid arthritis. It  
 XX is also useful against cell surface antigens and antibodies reactive  
 XX against cell surface antigens can be used for diagnostic  
 XX reagents. The process allows antibodies to be raised against  
 XX antigens which are present in very low amounts or which are  
 XX difficult to purify. The process also allows the use of large numbers  
 XX of hybridomas and without requiring high purity antigens for enrichment.  
 XX  
 XX Sequence 13 AA:  
 XX  
 XX Query Match 100.0%; Score 44; DB 19; Length 15;  
 XX Best Local Similarity 100.0%; Pred. No. 0.027;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 27 1 FOREPTLAS 9  
 XX 1 FOREPTLAS 5  
 XX  
 XX RESULT 8  
 XX W0200214870-A1.  
 XX 10-AMN1539 standard: peptide: 16 AA.  
 XX  
 XX AKMS1539:  
 XX 28-APR-1998 (first entry)  
 XX Human cartilage glycoprotein 39 derived peptide #40.  
 XX  
 XX Articular cartilage: immunosuppressive therapy; antigen; autoantigen;  
 XX immunological tolerance; T-cell; human cartilage glycoprotein 39;  
 XX HC 3P-39; Rheumatoid arthritis; epitope.  
 XX  
 XX Synthetic.  
 XX OS Homo sapiens.  
 XX WO9740068-A1.  
 XX 30-OCT-1997.  
 XX 22-APR-1997: 97MO-EPO2051.  
 XX 24-APR-1996: 96EP-020106.  
 XX (AKU) AKZO NOBEL NV.  
 XX Boots AMB, Verheijden GPH.  
 XX WPI: 1997-537775/49.  
 XX  
 XX Peptide suitable for use in antigen specific immunosuppressive  
 XX therapy. The peptide is derived from the sequence of the  
 XX inducing systemic immunological tolerance to rheumatoid arthritis  
 XX autoantigen.  
 XX  
 XX Disclosure: Page 16; 82pp: English.  
 XX  
 XX The present sequence represents a peptide which resembles or mimics an  
 XX epitope present on human cartilage glycoprotein 39 (HC 3p-39), an







FT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis

XX Claim 17: Fig 55: 134pp: English.  
 CC The sequence represents synthetic human multi-target autoantigen  
 CC (EMULATING) Y-RNA consisting of regions encoding  $\alpha$ 2(I)collagen/RA,  
 CC  $\alpha$ 1(I)collagen,  $\alpha$ 2(I)collagen,  $\alpha$ 1(II)collagen,  $\alpha$ 2(II)collagen,  $\alpha$ 1(III)collagen,  
 CC of the invention comprising sequences coding for at least a part of  
 CC autoantigens related to a specific autoimmune disease. The synthetic  
 CC sequences are fused to a specific autoantigen, such as human  
 CC diabetes with as multiple epitopes, brain-independent diabetes  
 CC mellitus, rheumatoid arthritis, myasthenia gravis, uveitis, autoimmune  
 CC thyroiditis, Sjogren's syndrome, idiopathic thrombocytopenic  
 CC purpura, and inflammatory diseases.  $\alpha$ 2(I)collagen,  $\alpha$ 1(II)collagen,  
 CC the synthetic human target autoantigen genes are also useful for  
 CC diagnosis and/or monitoring the progression of the autoimmune disease.

XX Sequence 350 AA:

Query Match 100.0% Score 41, DB 22, Length 100  
 Best Local Similarity 100.0% Pred No 0.79  
 Matches 9; Conservative 0; Mismatches 0; Indels 0, 25pp 0.

OY 1 F0RSTPLAS 9

DB 272 F0RSTPLAS 250

REMARK 13

AMR03442

ID AMR03442 standard; Protein: 381 AA.

XX AMR03442:

OY 01-JAN-2001 (first entry)

DE Gp38k protein sequence.

XX Gp38k, chemotactant, cell migration, wound healing; angiogenesis;

XX cancer; vascular trauma; vascular disease; atherosclerosis; retinosis;

XX unidentified.

XX Key Location/Qualifiers

FT Peptide 17-24

FT /label: signal\_peptide

FT Region 30-37

FT /note: "peptide antibody"

FT Modified-site 68-75

FT /label: glycosylation\_site

FT Binding-site 68-75

FT /label: zinc\_finger

FT Binding-site 68-75

FT /label: leucine zipper

FT Active-site 116-116

FT /label: catalytic\_site

FT Binding-site 143-146

FT /label: chitinase\_active\_site

FT Binding-site 143-146

FT /label: heparin\_binding\_site

FT Binding-site 143-146

FT /label: hyaluronic\_acid\_binding\_site

FT Binding-site 262-270

FT /label: hyaluronic\_acid\_binding\_site

FT Binding-site 278-281

FT /label: hyaluronic\_acid\_binding\_site

FT Binding-site 282-290

FT /label: glycosaminoglycan\_binding\_site

FT Region: 74-95

FT /label: acidic\_region

FT Binding-site 358-376

FT /label: hyaluronic\_acid\_binding\_site

PM M0200034469-M1

XX 15-JUN-2000.

XX 10-DEC-1999: 3900-US29262.  
 XX 11-DEC-1998: 3905-011856.  
 XX 11-DEC-1998: 3905-011856.  
 XX (UNIK ) UNIV NEW YORK STATE RES FUND.

XX Mills AMT;

XX WFL: 4000-431300/37

XX Clusterin and gp38k-related peptide capable of altering cell migration;  
 XX useful for treating atherosclerosis, cancer and sclerosis following  
 XX vascular trauma or disease.  
 XX U-closure; Fig 2, 4pp: English.

XX The present sequence is the protein sequence of gp38k, gp38k, a  
 XX chemotactant, is essential for the development of the smooth  
 XX muscle (VSMC). The gene and protein can, therefore, be used to promote  
 XX wound healing, angiogenesis and vasculogenesis. In the treatment of  
 XX atherosclerosis, and anti-atherosclerotic agents, the use of gp38k, as  
 XX chemotactant, and anti-atherosclerotic agents can be used to treat cancer, as  
 XX angiogenesis is vital for tumor survival.

XX Sequence 383 AA:

Query Match 100.0% Score 41, DB 21, Length 383

Best Local Similarity 100.0% Pred No 0.79

Matches 9; Conservative 0; Mismatches 0; Indels 0, Gaps 0;

OY 1 F0RSTPLAS 9

DE 461 F0RSTPLAS 269

REMARK 14

AMR03927

ID AMR03927 standard; Protein: 383 AA.

XX AMR03927:

OY 11-DEC-2002 (first entry)

DE Human ovarian cancer marker

XX Human ovarian cancer marker; cancer familial history; brain disorder;

XX Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;

XX brain herniation; inflammation; encephalitis; testicular disorder;

XX heart disorder; ischemic heart disease; atherosclerosis; neoplasia;

XX histological type; carcinogenic; ovarian cancer marker.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

PI Meyers RE, Morrissy MP, Clendy RJ, Son A, Viskay PO, Mills GB;  
 PI Bat SC, Lu K, Schmidt RE, Zhao X, Galt K;  
 XX NPI: 200272327/76.  
 DR N-PSB: AB574389.  
 XX Assessing whether a patient is afflicted with ovarian cancer, useful in  
 XX assessing the stage or progression of the disease, comprises: using  
 XX the expression level of a cancer marker in a sample from a patient and  
 XX from a non cancer patient."

PS Disclosure: Page 164-165: 48PP: English.

CC The present invention relates to a new method for assessing whether a  
 CC patient is afflicted with ovarian cancer. The method involves comparing  
 CC the expression level of a marker in a patient sample and the normal level  
 CC of the marker. The marker is selected from 363 cancer markers described in the  
 CC specification. The method of the invention is useful in diagnosing or  
 CC specifying the stage or progression of the disease, and also in assessing  
 CC the possibility, and the recurrence of ovarian cancer. The method may also be of  
 CC particular use with patients having an enhanced risk of developing  
 CC ovarian cancer. The cancer markers may be used in the diagnosis and treatment  
 CC of e.g. brain and central nervous system disorders (e.g. bacterial and  
 CC meningitis, Alzheimer's disease or Parkinson's disease), brain  
 CC inflammations (e.g. bacterial or viral; dermatitis or encephalitis),  
 CC testicular disorders (e.g. noncancerous granulomatous orchitis), test  
 CC disease or atrophic orchitis). The compositions and methods may also be  
 CC used in assessing the histological type of neoplasia associated with  
 CC ovarian cancer. The method may also be used in determining whether ovarian  
 CC cancer is metastasizing, selecting a composition for inhibiting ovarian cancer,  
 CC inhibiting ovarian cancer or at risk of developing ovarian cancer. The  
 CC present amino acid sequence represents one of the ovarian cancer markers  
 CC described in the invention.

XX Sequence 381 AA.

Query Match 120.0% Score 44; DS 23; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 0.7%  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VESTRLAS 9  
 1111111111  
 261 FOSSTPLAS 265

REUSIT 25  
 AB55651  
 ID AB056551 Standard; Protein: 363 AA.

AC AB056551;

XX 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide r244.

XX Lung cancer-associated polypeptide; detection: epifluorescence;  
 XX anti-inflammatory; anti-inflammatory; non-small cell lung cancer; stercocystis;  
 XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 XX intestinal pulmonary fibrosis; fibroses; asthma bronchocystis.

XX Unidentified.

XX M020026443-A2.

XX 31-OCT-2002.

XX 18-APR-2002: 2002MO-0312476.  
 XX 18-APR-2001: 2001US-384770P.  
 XX 09-NOV-2001: 2001US-339244P.  
 XX 09-NOV-2001: 2001US-339244P.  
 XX 13-NOV-2001: 2001US-306666P.  
 XX 13-NOV-2001: 2001US-306666P.  
 XX 12-NOV-2001: 2002US-722446.  
 XX (EUSB) EUS BIOTECHNOLOGY INC.

PI Aziz K, Murray R;

XX WPI: 2002-09115/08  
 DR N-PSB: AB576340.

XX Possessing a lung cancer-associated transcript in a cell from a patient  
 XX for treating lung cancer, by contacting a biological sample from the  
 XX patient with a polynucleotide that exhibits increased or decreased  
 XX expression in lung cancer.

XX Claim 27; page 177; 453pp: English.

CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridizes  
 CC to the transcript, and detecting the hybridization product. The method  
 CC increased or decreased expression in lung cancer samples. Lung  
 CC cancer-associated polynucleotides and polypeptides are used for  
 CC polypeptide for inhibiting proliferation of a lung cancer-associated  
 CC cell to treat lung cancer in a patient and for treating a mammal having  
 CC cancer, non-small cell lung cancer or other benign or precancerous  
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, metastatic  
 CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides  
 CC and polypeptides are useful for diagnostic purposes and as antigens for  
 CC antibodies. The genes, polynucleotides and polypeptides are also useful for  
 CC antibodies. Sequences AB056408-AB056745 represent lung cancer-associated  
 CC polypeptides of the invention.

XX Sequence 381 AA;

Query Match 100.0% Score 44; DW 24; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 0.7%  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGSSTPLAS 9  
 1111111111  
 261 FOSSTPLAS 269

Search completed: September 24, 2003, 13:41:15  
 Run time: 31.256 secs

BioEdit version 5.1.6

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OM protein - protein search, using sv model

Run on: September 24, 2003, 13:35:21, Search time 16.6913 seconds

[align] alignments: 35,667 Million cals: -1048.05/sec

File: us-09-744-282-1

Perfect score: 44

Sequence: 1 PERSPTLAS 9

Scoring table: BLOSUM62

Gapop 11.0, Gapeat 0.5

Searched: 128717 seqs, 4210855 resids.wts

Total number of hits satisfying chosen parameters: 128717

Minimum DB seq length: 0

Maximum DB seq length: 2500000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Printing: Fasta 10 summaries

Database:

1: /usr/local/seqs/AA

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3: /usr2/ptdata/1/aa/CA.COMB pep \*

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2 GENERAL INFORMATION:
3 APPLICANT: A.M. Boots
4 APPLICANT: A.M. Boots
5 APPLICANT: U.S. Biotech
6 APPLICANT: U.S. Biotech
7 TITLE OF INVENTION: No. 5843449el Peptides derived from autoantigen for use
8 in the treatment of autoimmune diseases
9 NUMBER OF SEQUENCES: 10 Immunotherapy of Autoimmune Diseases
10 CURRENT APPLICATION DATA:
11 CORRESPONDENCE ADDRESS:
12 ADDRESS: 1300 Piccard Drive, Suite 200
13 CITY: Rockville
14 STATE: Maryland
15 COUNTRY: U.S.A.
16 ZIP: 20850
17 COMPUTER READABLE FORM:
18 OPERATING SYSTEM: IBM PC compatible
19 OPERATING SYSTEM: IBM PC compatible
20 OPERATING SYSTEM: IBM PC compatible
21 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0 (EPO)
22 CURRENT APPLICATION DATA: 05/06/19, 645
23 FILING DATE: 25-MAR-1995
24 CLASSIFICATION: 5:24
25 PRIORITY CLAIM:
26 NAME: Corley, Mary E.
27 REGISTRATION NUMBER: 34,405
28 TELEPHONE: (301) 447-4433
29 INFORMATION FOR SEQ ID NO: 1:
30 SEQUENCE CHARACTERISTICS:
31 TYPE: amino acid
32 STRAND: single
33 TRANSDUCED: no
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45 GENERAL INFORMATION:
46 APPLICANT: A.M. Boots
47 APPLICANT: A.M. Boots
48 APPLICANT: U.S. Biotech
49 APPLICANT: U.S. Biotech
50 TITLE OF INVENTION: No. 5843449el Peptides derived from autoantigen for use
51 in the treatment of autoimmune diseases
52 NUMBER OF SEQUENCES: 10 Immunotherapy of Autoimmune Diseases
53 CORRESPONDENCE ADDRESS: 5843449el Patent Department
54 ADDRESS: 1300 Piccard Drive, Suite 200
55 CITY: Rockville
56 STATE: Maryland
57 COUNTRY: U.S.A.
58 ZIP: 20850
59 COMPUTER READABLE FORM:
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64 CURRENT APPLICATION DATA:
65 CORRESPONDENCE ADDRESS: 05/06/19, 645
66 FILING DATE: 25-MAR-1995
67 APPLICATION NUMBER: US 08/619,645
68 PRIORITY CLAIM:
69 FILING DATE: 25-MAR-1995
70 FILING DATE: 27-OCT-1994
71 FILING DATE: 27-OCT-1994
72 FILING DATE: 07-APR-1995
73 TELEPHONE: (301) 508-7206
74 INFORMATION FOR SEQ ID NO: 1:
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76 TYPE: amino acid
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87 RESULT 3
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89 Sequence 5: Application US/08619645
90 GENERAL INFORMATION:
91 APPLICANT: A.M. Boots
92 APPLICANT: A.M. Boots
93 APPLICANT: U.S. Biotech
94 APPLICANT: U.S. Biotech
95 TITLE OF INVENTION: No. 5716507el Peptides derived from
96 in the treatment of autoimmune diseases
97 NUMBER OF SEQUENCES: 9
98 CORRESPONDENCE ADDRESS:
99 ADDRESS: 1300 Piccard Drive, Suite 200
100 CITY: Rockville
101 STATE: Maryland
102 COUNTRY: U.S.A.
103 ZIP: 20850
104 COMPUTER READABLE FORM:
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107 OPERATING SYSTEM: IBM PC compatible
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110 CORRESPONDENCE ADDRESS: 05/06/19, 645
111 FILING DATE: 25-MAR-1995
112 APPLICATION NUMBER: US 08/619,645
113 PRIORITY CLAIM:
114 FILING DATE: 25-MAR-1995
115 FILING DATE: 27-OCT-1994
116 FILING DATE: 27-OCT-1994
117 FILING DATE: 07-APR-1995
118 TELEPHONE: (301) 508-7206
119 INFORMATION FOR SEQ ID NO: 1:
120 SEQUENCE CHARACTERISTICS:
121 TYPE: amino acid
122 STRAND: single
123 TRANSDUCED: no
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126 Query Match
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128 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
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134 Sequence 5: Application US/08619645
135 GENERAL INFORMATION:
136 APPLICANT: A.M. Boots
137 APPLICANT: A.M. Boots
138 APPLICANT: U.S. Biotech
139 APPLICANT: U.S. Biotech
140 TITLE OF INVENTION: No. 5716507el Peptides derived from
141 in the treatment of autoimmune diseases
142 NUMBER OF SEQUENCES: 9
143 CORRESPONDENCE ADDRESS:
144 ADDRESS: 1300 Piccard Drive, Suite 200
145 CITY: Rockville
146 STATE: Maryland
147 COUNTRY: U.S.A.
148 ZIP: 20850
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153 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
154 CURRENT APPLICATION DATA:
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156 FILING DATE: 25-MAR-1995
157 APPLICATION NUMBER: US 08/619,645
158 PRIORITY CLAIM:
159 FILING DATE: 25-MAR-1995
160 FILING DATE: 27-OCT-1994
161 FILING DATE: 27-OCT-1994
162 FILING DATE: 07-APR-1995
163 TELEPHONE: (301) 508-7206
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166 TYPE: amino acid
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178 US-08-619-645-5
179 Sequence 5: Application US/08619645
180 GENERAL INFORMATION:
181 APPLICANT: A.M. Boots
182 APPLICANT: A.M. Boots
183 APPLICANT: U.S. Biotech
184 APPLICANT: U.S. Biotech
185 TITLE OF INVENTION: No. 5716507el Peptides derived from
186 in the treatment of autoimmune diseases
187 NUMBER OF SEQUENCES: 9
188 CORRESPONDENCE ADDRESS:
189 ADDRESS: 1300 Piccard Drive, Suite 200
190 CITY: Rockville
191 STATE: Maryland
192 COUNTRY: U.S.A.
193 ZIP: 20850
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198 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
199 CURRENT APPLICATION DATA:
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201 FILING DATE: 25-MAR-1995
202 APPLICATION NUMBER: US 08/619,645
203 PRIORITY CLAIM:
204 FILING DATE: 25-MAR-1995
205 FILING DATE: 27-OCT-1994
206 FILING DATE: 27-OCT-1994
207 FILING DATE: 07-APR-1995
208 TELEPHONE: (301) 508-7206
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212 STRAND: single
213 TRANSDUCED: no
214 MOLECULE TYPE: peptide
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224 Sequence 5: Application US/08619645
225 GENERAL INFORMATION:
226 APPLICANT: A.M. Boots
227 APPLICANT: A.M. Boots
228 APPLICANT: U.S. Biotech
229 APPLICANT: U.S. Biotech
230 TITLE OF INVENTION: No. 5716507el Peptides derived from
231 in the treatment of autoimmune diseases
232 NUMBER OF SEQUENCES: 9
233 CORRESPONDENCE ADDRESS:
234 ADDRESS: 1300 Piccard Drive, Suite 200
235 CITY: Rockville
236 STATE: Maryland
237 COUNTRY: U.S.A.
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246 FILING DATE: 25-MAR-1995
247 APPLICATION NUMBER: US 08/619,645
248 PRIORITY CLAIM:
249 FILING DATE: 25-MAR-1995
250 FILING DATE: 27-OCT-1994
251 FILING DATE: 27-OCT-1994
252 FILING DATE: 07-APR-1995
253 TELEPHONE: (301) 508-7206
254 INFORMATION FOR SEQ ID NO: 1:
255 SEQUENCE CHARACTERISTICS:
256 TYPE: amino acid
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269 Sequence 5: Application US/08619645
270 GENERAL INFORMATION:
271 APPLICANT: A.M. Boots
272 APPLICANT: A.M. Boots
273 APPLICANT: U.S. Biotech
274 APPLICANT: U.S. Biotech
275 TITLE OF INVENTION: No. 5716507el Peptides derived from
276 in the treatment of autoimmune diseases
277 NUMBER OF SEQUENCES: 9
278 CORRESPONDENCE ADDRESS:
279 ADDRESS: 1300 Piccard Drive, Suite 200
280 CITY: Rockville
281 STATE: Maryland
282 COUNTRY: U.S.A.
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285 OPERATING SYSTEM: IBM PC compatible
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314 Sequence 5: Application US/08619645
315 GENERAL INFORMATION:
316 APPLICANT: A.M. Boots
317 APPLICANT: A.M. Boots
318 APPLICANT: U.S. Biotech
319 APPLICANT: U.S. Biotech
320 TITLE OF INVENTION: No. 5716507el Peptides derived from
321 in the treatment of autoimmune diseases
322 NUMBER OF SEQUENCES: 9
323 CORRESPONDENCE ADDRESS:
324 ADDRESS: 1300 Piccard Drive, Suite 200
325 CITY: Rockville
326 STATE: Maryland
327 COUNTRY: U.S.A.
328 ZIP: 20850
329 COMPUTER READABLE FORM:
330 OPERATING SYSTEM: IBM PC compatible
331 OPERATING SYSTEM: IBM PC compatible
332 OPERATING SYSTEM: IBM PC compatible
333 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
334 CURRENT APPLICATION DATA:
335 CORRESPONDENCE ADDRESS: 05/06/19, 645
336 FILING DATE: 25-MAR-1995
337 APPLICATION NUMBER: US 08/619,645
338 PRIORITY CLAIM:
339 FILING DATE: 25-MAR-1995
340 FILING DATE: 27-OCT-1994
341 FILING DATE: 27-OCT-1994
342 FILING DATE: 07-APR-1995
343 TELEPHONE: (301) 508-7206
344 INFORMATION FOR SEQ ID NO: 1:
345 SEQUENCE CHARACTERISTICS:
346 TYPE: amino acid
347 STRAND: single
348 TRANSDUCED: no
349 MOLECULE TYPE: peptide
350 US-08-634-493-1
351 Query Match
352 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
353 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
354 07 1 F08SF7LAS 9
355 08 1 F08SF7LAS 9
356
357 RESULT 3
358 US-08-619-645-5
359 Sequence 5: Application US/08619645
360 GENERAL INFORMATION:
361 APPLICANT: A.M. Boots
362 APPLICANT: A.M. Boots
363 APPLICANT: U.S. Biotech
364 APPLICANT: U.S. Biotech
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384 FILING DATE: 25-MAR-1995
385 FILING DATE: 27-OCT-1994
386 FILING DATE: 27-OCT-1994
387 FILING DATE: 07-APR-1995
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393 TRANSDUCED: no
394 MOLECULE TYPE: peptide
395 US-08-634-493-1
396 Query Match
397 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
398 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
399 07 1 F08SF7LAS 9
400 08 1 F08SF7LAS 9
401
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403 US-08-619-645-5
404 Sequence 5: Application US/08619645
405 GENERAL INFORMATION:
406 APPLICANT: A.M. Boots
407 APPLICANT: A.M. Boots
408 APPLICANT: U.S. Biotech
409 APPLICANT: U.S. Biotech
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420 OPERATING SYSTEM: IBM PC compatible
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422 OPERATING SYSTEM: IBM PC compatible
423 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
424 CURRENT APPLICATION DATA:
425 CORRESPONDENCE ADDRESS: 05/06/19, 645
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427 APPLICATION NUMBER: US 08/619,645
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429 FILING DATE: 25-MAR-1995
430 FILING DATE: 27-OCT-1994
431 FILING DATE: 27-OCT-1994
432 FILING DATE: 07-APR-1995
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437 STRAND: single
438 TRANSDUCED: no
439 MOLECULE TYPE: peptide
440 US-08-634-493-1
441 Query Match
442 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
443 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
444 07 1 F08SF7LAS 9
445 08 1 F08SF7LAS 9
446
447 RESULT 3
448 US-08-619-645-5
449 Sequence 5: Application US/08619645
450 GENERAL INFORMATION:
451 APPLICANT: A.M. Boots
452 APPLICANT: A.M. Boots
453 APPLICANT: U.S. Biotech
454 APPLICANT: U.S. Biotech
455 TITLE OF INVENTION: No. 5716507el Peptides derived from
456 in the treatment of autoimmune diseases
457 NUMBER OF SEQUENCES: 9
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459 ADDRESS: 1300 Piccard Drive, Suite 200
460 CITY: Rockville
461 STATE: Maryland
462 COUNTRY: U.S.A.
463 ZIP: 20850
464 COMPUTER READABLE FORM:
465 OPERATING SYSTEM: IBM PC compatible
466 OPERATING SYSTEM: IBM PC compatible
467 OPERATING SYSTEM: IBM PC compatible
468 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
469 CURRENT APPLICATION DATA:
470 CORRESPONDENCE ADDRESS: 05/06/19, 645
471 FILING DATE: 25-MAR-1995
472 APPLICATION NUMBER: US 08/619,645
473 PRIORITY CLAIM:
474 FILING DATE: 25-MAR-1995
475 FILING DATE: 27-OCT-1994
476 FILING DATE: 27-OCT-1994
477 FILING DATE: 07-APR-1995
478 TELEPHONE: (301) 508-7206
479 INFORMATION FOR SEQ ID NO: 1:
480 SEQUENCE CHARACTERISTICS:
481 TYPE: amino acid
482 STRAND: single
483 TRANSDUCED: no
484 MOLECULE TYPE: peptide
485 US-08-634-493-1
486 Query Match
487 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
488 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
489 07 1 F08SF7LAS 9
490 08 1 F08SF7LAS 9
491
492 RESULT 3
493 US-08-619-645-5
494 Sequence 5: Application US/08619645
495 GENERAL INFORMATION:
496 APPLICANT: A.M. Boots
497 APPLICANT: A.M. Boots
498 APPLICANT: U.S. Biotech
499 APPLICANT: U.S. Biotech
500 TITLE OF INVENTION: No. 5716507el Peptides derived from
501 in the treatment of autoimmune diseases
502 NUMBER OF SEQUENCES: 9
503 CORRESPONDENCE ADDRESS:
504 ADDRESS: 1300 Piccard Drive, Suite 200
505 CITY: Rockville
506 STATE: Maryland
507 COUNTRY: U.S.A.
508 ZIP: 20850
509 COMPUTER READABLE FORM:
510 OPERATING SYSTEM: IBM PC compatible
511 OPERATING SYSTEM: IBM PC compatible
512 OPERATING SYSTEM: IBM PC compatible
513 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
514 CURRENT APPLICATION DATA:
515 CORRESPONDENCE ADDRESS: 05/06/19, 645
516 FILING DATE: 25-MAR-1995
517 APPLICATION NUMBER: US 08/619,645
518 PRIORITY CLAIM:
519 FILING DATE: 25-MAR-1995
520 FILING DATE: 27-OCT-1994
521 FILING DATE: 27-OCT-1994
522 FILING DATE: 07-APR-1995
523 TELEPHONE: (301) 508-7206
524 INFORMATION FOR SEQ ID NO: 1:
525 SEQUENCE CHARACTERISTICS:
526 TYPE: amino acid
527 STRAND: single
528 TRANSDUCED: no
529 MOLECULE TYPE: peptide
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531 Query Match
532 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
533 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
534 07 1 F08SF7LAS 9
535 08 1 F08SF7LAS 9
536
537 RESULT 3
538 US-08-619-645-5
539 Sequence 5: Application US/08619645
540 GENERAL INFORMATION:
541 APPLICANT: A.M. Boots
542 APPLICANT: A.M. Boots
543 APPLICANT: U.S. Biotech
544 APPLICANT: U.S. Biotech
545 TITLE OF INVENTION: No. 5716507el Peptides derived from
546 in the treatment of autoimmune diseases
547 NUMBER OF SEQUENCES: 9
548 CORRESPONDENCE ADDRESS:
549 ADDRESS: 1300 Piccard Drive, Suite 200
550 CITY: Rockville
551 STATE: Maryland
552 COUNTRY: U.S.A.
553 ZIP: 20850
554 COMPUTER READABLE FORM:
555 OPERATING SYSTEM: IBM PC compatible
556 OPERATING SYSTEM: IBM PC compatible
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558 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
559 CURRENT APPLICATION DATA:
560 CORRESPONDENCE ADDRESS: 05/06/19, 645
561 FILING DATE: 25-MAR-1995
562 APPLICATION NUMBER: US 08/619,645
563 PRIORITY CLAIM:
564 FILING DATE: 25-MAR-1995
565 FILING DATE: 27-OCT-1994
566 FILING DATE: 27-OCT-1994
567 FILING DATE: 07-APR-1995
568 TELEPHONE: (301) 508-7206
569 INFORMATION FOR SEQ ID NO: 1:
570 SEQUENCE CHARACTERISTICS:
571 TYPE: amino acid
572 STRAND: single
573 TRANSDUCED: no
574 MOLECULE TYPE: peptide
575 US-08-634-493-1
576 Query Match
577 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
578 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
579 07 1 F08SF7LAS 9
580 08 1 F08SF7LAS 9
581
582 RESULT 3
583 US-08-619-645-5
584 Sequence 5: Application US/08619645
585 GENERAL INFORMATION:
586 APPLICANT: A.M. Boots
587 APPLICANT: A.M. Boots
588 APPLICANT: U.S. Biotech
589 APPLICANT: U.S. Biotech
590 TITLE OF INVENTION: No. 5716507el Peptides derived from
591 in the treatment of autoimmune diseases
592 NUMBER OF SEQUENCES: 9
593 CORRESPONDENCE ADDRESS:
594 ADDRESS: 1300 Piccard Drive, Suite 200
595 CITY: Rockville
596 STATE: Maryland
597 COUNTRY: U.S.A.
598 ZIP: 20850
599 COMPUTER READABLE FORM:
600 OPERATING SYSTEM: IBM PC compatible
601 OPERATING SYSTEM: IBM PC compatible
602 OPERATING SYSTEM: IBM PC compatible
603 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
604 CURRENT APPLICATION DATA:
605 CORRESPONDENCE ADDRESS: 05/06/19, 645
606 FILING DATE: 25-MAR-1995
607 APPLICATION NUMBER: US 08/619,645
608 PRIORITY CLAIM:
609 FILING DATE: 25-MAR-1995
610 FILING DATE: 27-OCT-1994
611 FILING DATE: 27-OCT-1994
612 FILING DATE: 07-APR-1995
613 TELEPHONE: (301) 508-7206
614 INFORMATION FOR SEQ ID NO: 1:
615 SEQUENCE CHARACTERISTICS:
616 TYPE: amino acid
617 STRAND: single
618 TRANSDUCED: no
619 MOLECULE TYPE: peptide
620 US-08-634-493-1
621 Query Match
622 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
623 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
624 07 1 F08SF7LAS 9
625 08 1 F08SF7LAS 9
626
627 RESULT 3
628 US-08-619-645-5
629 Sequence 5: Application US/08619645
630 GENERAL INFORMATION:
631 APPLICANT: A.M. Boots
632 APPLICANT: A.M. Boots
633 APPLICANT: U.S. Biotech
634 APPLICANT: U.S. Biotech
635 TITLE OF INVENTION: No. 5716507el Peptides derived from
636 in the treatment of autoimmune diseases
637 NUMBER OF SEQUENCES: 9
638 CORRESPONDENCE ADDRESS:
639 ADDRESS: 1300 Piccard Drive, Suite 200
640 CITY: Rockville
641 STATE: Maryland
642 COUNTRY: U.S.A.
643 ZIP: 20850
644 COMPUTER READABLE FORM:
645 OPERATING SYSTEM: IBM PC compatible
646 OPERATING SYSTEM: IBM PC compatible
647 OPERATING SYSTEM: IBM PC compatible
648 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
649 CURRENT APPLICATION DATA:
650 CORRESPONDENCE ADDRESS: 05/06/19, 645
651 FILING DATE: 25-MAR-1995
652 APPLICATION NUMBER: US 08/619,645
653 PRIORITY CLAIM:
654 FILING DATE: 25-MAR-1995
655 FILING DATE: 27-OCT-1994
656 FILING DATE: 27-OCT-1994
657 FILING DATE: 07-APR-1995
658 TELEPHONE: (301) 508-7206
659 INFORMATION FOR SEQ ID NO: 1:
660 SEQUENCE CHARACTERISTICS:
661 TYPE: amino acid
662 STRAND: single
663 TRANSDUCED: no
664 MOLECULE TYPE: peptide
665 US-08-634-493-1
666 Query Match
667 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
668 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
669 07 1 F08SF7LAS 9
670 08 1 F08SF7LAS 9
671
672 RESULT 3
673 US-08-619-645-5
674 Sequence 5: Application US/08619645
675 GENERAL INFORMATION:
676 APPLICANT: A.M. Boots
677 APPLICANT: A.M. Boots
678 APPLICANT: U.S. Biotech
679 APPLICANT: U.S. Biotech
680 TITLE OF INVENTION: No. 5716507el Peptides derived from
681 in the treatment of autoimmune diseases
682 NUMBER OF SEQUENCES: 9
683 CORRESPONDENCE ADDRESS:
684 ADDRESS: 1300 Piccard Drive, Suite 200
685 CITY: Rockville
686 STATE: Maryland
687 COUNTRY: U.S.A.
688 ZIP: 20850
689 COMPUTER READABLE FORM:
690 OPERATING SYSTEM: IBM PC compatible
691 OPERATING SYSTEM: IBM PC compatible
692 OPERATING SYSTEM: IBM PC compatible
693 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
694 CURRENT APPLICATION DATA:
695 CORRESPONDENCE ADDRESS: 05/06/19, 645
696 FILING DATE: 25-MAR-1995
697 APPLICATION NUMBER: US 08/619,645
698 PRIORITY CLAIM:
699 FILING DATE: 25-MAR-1995
700 FILING DATE: 27-OCT-1994
701 FILING DATE: 27-OCT-1994
702 FILING DATE: 07-APR-1995
703 TELEPHONE: (301) 508-7206
704 INFORMATION FOR SEQ ID NO: 1:
705 SEQUENCE CHARACTERISTICS:
706 TYPE: amino acid
707 STRAND: single
708 TRANSDUCED: no
709 MOLECULE TYPE: peptide
710 US-08-634-493-1
711 Query Match
712 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
713 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
714 07 1 F08SF7LAS 9
715 08 1 F08SF7LAS 9
716
717 RESULT 3
718 US-08-619-645-5
719 Sequence 5: Application US/08619645
720 GENERAL INFORMATION:
721 APPLICANT: A.M. Boots
722 APPLICANT: A.M. Boots
723 APPLICANT: U.S. Biotech
724 APPLICANT: U.S. Biotech
725 TITLE OF INVENTION: No. 5716507el Peptides derived from
726 in the treatment of autoimmune diseases
727 NUMBER OF SEQUENCES: 9
728 CORRESPONDENCE ADDRESS:
729 ADDRESS: 1300 Piccard Drive, Suite 200
730 CITY: Rockville
731 STATE: Maryland
732 COUNTRY: U.S.A.
733 ZIP: 20850
734 COMPUTER READABLE FORM:
735 OPERATING SYSTEM: IBM PC compatible
736 OPERATING SYSTEM: IBM PC compatible
737 OPERATING SYSTEM: IBM PC compatible
738 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
739 CURRENT APPLICATION DATA:
740 CORRESPONDENCE ADDRESS: 05/06/19, 645
741 FILING DATE: 25-MAR-1995
742 APPLICATION NUMBER: US 08/619,645
743 PRIORITY CLAIM:
744 FILING DATE: 25-MAR-1995
745 FILING DATE: 27-OCT-1994
746 FILING DATE: 27-OCT-1994
747 FILING DATE: 07-APR-1995
748 TELEPHONE: (301) 508-7206
749 INFORMATION FOR SEQ ID NO: 1:
750 SEQUENCE CHARACTERISTICS:
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752 STRAND: single
753 TRANSDUCED: no
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756 Query Match
757 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
758 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
759 07 1 F08SF7LAS 9
760 08 1 F08SF7LAS 9
761
762 RESULT 3
763 US-08-619-645-5
764 Sequence 5: Application US/08619645
765 GENERAL INFORMATION:
766 APPLICANT: A.M. Boots
767 APPLICANT: A.M. Boots
768 APPLICANT: U.S. Biotech
769 APPLICANT: U.S. Biotech
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771 in the treatment of autoimmune diseases
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779 COMPUTER READABLE FORM:
780 OPERATING SYSTEM: IBM PC compatible
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782 OPERATING SYSTEM: IBM PC compatible
783 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
784 CURRENT APPLICATION DATA:
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786 FILING DATE: 25-MAR-1995
787 APPLICATION NUMBER: US 08/619,645
788 PRIORITY CLAIM:
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807 RESULT 3
808 US-08-619-645-5
809 Sequence 5: Application US/08619645
810 GENERAL INFORMATION:
811 APPLICANT: A.M. Boots
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813 APPLICANT: U.S. Biotech
814 APPLICANT: U.S. Biotech
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822 COUNTRY: U.S.A.
823 ZIP: 20850
824 COMPUTER READABLE FORM:
825 OPERATING SYSTEM: IBM PC compatible
826 OPERATING SYSTEM: IBM PC compatible
827 OPERATING SYSTEM: IBM PC compatible
828 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
829 CURRENT APPLICATION DATA:
830 CORRESPONDENCE ADDRESS: 05/06/19, 645
831 FILING DATE: 25-MAR-1995
832 APPLICATION NUMBER: US 08/619,645
833 PRIORITY CLAIM:
834 FILING DATE: 25-MAR-1995
835 FILING DATE: 27-OCT-1994
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846 Query Match
847 Best Local Similarity 100.0%, Score 41; DB 2; Length 9;
848 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
849 07 1 F08SF7LAS 9
850 08 1 F08SF7LAS 9
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852 RESULT 3
853 US-08-619-645-5
854 Sequence 5: Application US/08619645
855 GENERAL INFORMATION:
856 APPLICANT: A.M. Boots
857 APPLICANT: A.M. Boots
858 APPLICANT: U.S. Biotech
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869 COMPUTER READABLE FORM:
870 OPERATING SYSTEM: IBM PC compatible
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873 SOFTWARE: PatentIn Release 4.1.0, Version 4.1.0
874 CURRENT APPLICATION DATA:
875 CORRESPONDENCE ADDRESS: 05/06/19, 645
876 FILING DATE: 25-MAR-1995
877 APPLICATION NUMBER: US 08/619,645
878 PRIORITY CLAIM:
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881 FILING DATE: 27-OCT-1994
882 FILING DATE: 07-APR-1995
883 TELEPHONE: (301) 508-7206
884 INFORMATION FOR SEQ ID NO: 1:
885 SEQUENCE CHARACTERISTICS:
886 TYPE: amino acid
887 STRAND: single
888 TRANSDUCED: no
889 MOLECULE TYPE: peptide
890 US-08-63
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GENERAL INFORMATION:  
 APPLICANT: Millio, Albert J.  
 TITLE OF INVENTION: Composition and Methods For Alleviating Cell Migration  
 CURRENT APPLICATION NUMBER: 09/794,455,749D  
 CURRENT FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: 07/111,856  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: PatentIn Ver. 2.1  
 LENGTH: 383  
 TYPE: PRT  
 US-09-45-749D-17

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 Best Local Similarity 100.0%, Pred. No. 0, 22, 0, Indels 0, Caps 0:  
 Matches 9: Conservative 0: Mismatches 0:

QY 1 F0RSTFLAS 9  
 DB 261 F0RSTFLAS 269

RESULT 9  
 US-09-039-198A-14  
 Sequence 14, Application US/0903198A  
 Patent No. 6200553  
 GENERAL INFORMATION:  
 APPLICANT: Gray, Patrick W.  
 TITLE OF INVENTION: CHINESE CHITIN-BINDING FRAGMENTS  
 NUMBER OF SEQ IDs: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gersquin, Murray & Botun  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60606-5402  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/09/03198A

Query Match 93.24, Score 41, DB 3, Length 373;  
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 QY 1 F0RSTFLAS 9  
 DB 246 F0RSTFLAS 254

US-09-039-198A-14  
 Sequence 14, Application US/0903198A  
 Patent No. 6200553  
 GENERAL INFORMATION:  
 APPLICANT: Gray, Patrick W.  
 TITLE OF INVENTION: CHINESE CHITIN-BINDING FRAGMENTS  
 NUMBER OF SEQ IDs: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gersquin, Murray & Botun  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60606-5402  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PatentIn Release #1.0, Version #1.22  
 CURRENT APPLICATION DATA:

RESULT 10  
 US-09-039-198A-15  
 Sequence 15, Application US/0903198A  
 Patent No. 6200553  
 GENERAL INFORMATION:  
 APPLICANT: Tjossem, Larry W.  
 TITLE OF INVENTION: CHINESE CHITIN-BINDING FRAGMENTS  
 NUMBER OF SEQ IDs: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gersquin, Murray & Botun  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60606-5402  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/09/039-198A

Query Match 93.24, Score 41, DB 3, Length 373;  
 Best Local Similarity 88.94, Pred. No. 0, 88, 0, Indels 0, Caps 0:  
 Matches 9: Conservative 1: Mismatches 0:  
 QY 1 F0RSTFLAS 9  
 DB 246 F0RSTFLAS 254

US-09-039-198A-15  
 Sequence 15, Application US/0903198A  
 Patent No. 6200553  
 GENERAL INFORMATION:  
 APPLICANT: Gray, Patrick W.  
 TITLE OF INVENTION: CHINESE CHITIN-BINDING FRAGMENTS  
 NUMBER OF SEQ IDs: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gersquin, Murray & Botun  
 CITY: Chicago  
 STATE: Illinois  
 ZIP: 60606-5402  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PatentIn Release #1.0, Version #1.22  
 CURRENT APPLICATION DATA:



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1 APPLICATION NUMBER: US/09/877,599
2 FILING DATE:
3 CLASSIFICATION: 514
4 PRIORITY: 88,941
5 APPLICATION NUMBER: US 39/463,618
6 FILING DATE: 15 JUN 1996
7 NAME: RUI LAURENCE; HIRSH
8 NAME: RUI LAURENCE; HIRSH
9 REGISTRATION NUMBER: 31,547
10 REFERENCE: 27866/33994
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 312/474 5300
13 TELEFAX: 312/474 5300
14 TELEFAX: 312/474 5300
15 INFORMATION FOR SEQ ID NO. 1:
16 SEQUENCE CHARACTERISTICS:
17 TYPE: amino acid
18 STRANDNESS: single
19 MOLECULE TYPE: peptide
20 US-09-877-599-11
21
22 Query Match 93.2%; Score 41; DB 4; Length 373;
23 Best Local Similarity 88.9%; Pred. No. 0.88;
24 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
25
26 QY 1 YGFSFTLAS 9
27
28 DB 246 YGFSFTLAS 254
29
30 RESULT 12
31 US-09-877-599-15
32
33 ? Sequence 15, Application US/0887599
34 ? Best Local Similarity 88.9%; Pred. No. 0.88;
35 ? Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
36
37 ? GENERAL INFORMATION:
38 ? APPLICANT: Gray, Patrick W.
39 ? TITLE OF INVENTION: On-line Materials and Methods
40 ? CORRESPONDENCE ADDRESS:
41 ? ADDRESSEE: Marshall, O'Toole, Gortton, Muray & Berman
42 ? STREET: 300 South Tower, 231 South Wacker Drive
43 ? CITY: Chicago
44 ? STATE: Illinois
45 ? ZIP: 60606-6402
46 ? COMPUTER READABLE FORM:
47 ? OPERATING SYSTEM: PC/IBM PC compatible
48 ? CURRENT APPLICATION NUMBER: US/09/877,599
49 ? FILING DATE: 514
50 ? PRIOR APPLICATION DATA:
51 ? APPLICATION NUMBER: US 08/663,618
52 ? FILING DATE: 1996
53 ? ATTORNEY/AGENT INFORMATION:
54 ? NAME: Rui-laurence, Li-hsueh
55 ? REGISTRATION NUMBER: 31,547
56 ? REFERENCE: 27866/33994
57 ? TELECOMMUNICATION INFORMATION:
58 ? TELEPHONE: 312/474 5300
59 ? TELEFAX: 312/474 5300
60 ? STRANDNESS: single
61 ? MOLECULE TYPE: amino acid
62 ? LENGTH: 373
63 ? INFORMATION FOR SEQ ID NO. 15:
64 ? SEQUENCE CHARACTERISTICS:
65 ? TYPE: amino acid
66 ? STRANDNESS: single
67 ? MOLECULE TYPE: peptide

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1 MOLECULE TYPE: peptide
2 US-09-877-599-15
3
4 Query Match 93.2%; Score 41; DB 4; Length 373;
5 Best Local Similarity 88.9%; Pred. No. 0.88;
6 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
7
8 QY 1 YGFSFTLAS 9
9
10 DB 246 YGFSFTLAS 254
11
12 RESULT 13
13 US-09-877-599-14
14
15 ? Sequence 14, Application US/0926574
16 ? Best Local Similarity 88.9%; Pred. No. 0.88;
17 ? Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
18
19 ? GENERAL INFORMATION:
20 ? APPLICANT: TIGLOR, JERRY K.
21 ? TITLE OF INVENTION: CHITIN-BINDING FRAGMENTS
22 ? CURRENT APPLICATION NUMBER: US/09/267,574
23 ? FILING DATE: 1998-03-12
24 ? EARLIER FILING DATE: 1998-03-12
25 ? NUMBER OF SEQ ID NOS: 39
26 ? MOLECULE TYPE: peptide
27 ? SEQ ID NO 1:
28 ? LYNPTPL 373
29 ? ORGANISM: Homo sapiens
30 ? ORGANISM: Homo sapiens
31 ? US-09-267-574-14
32
33 Query Match 93.2%; Score 41; DB 4; Length 373;
34 Best Local Similarity 88.9%; Pred. No. 0.88;
35 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
36
37 QY 1 YGFSFTLAS 9
38
39 DB 246 YGFSFTLAS 254
40
41 RESULT 14
42 US-09-267-574-15
43
44 ? Sequence 15, Application US/0946574
45 ? Best Local Similarity 88.9%; Pred. No. 0.88;
46 ? Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
47
48 ? GENERAL INFORMATION:
49 ? APPLICANT: JOSEPH, JERRY W.
50 ? TITLE OF INVENTION: CHITIN-BINDING FRAGMENTS
51 ? CURRENT APPLICATION NUMBER: US/09/267,574
52 ? FILING DATE: 1998-03-12
53 ? EARLIER FILING DATE: 1998-03-12
54 ? NUMBER OF SEQ ID NOS: 39
55 ? MOLECULE TYPE: peptide
56 ? SEQ ID NO 15:
57 ? LYNPTPL 373
58 ? ORGANISM: Homo sapiens
59 ? ORGANISM: Homo sapiens
60 ? US-09-267-574-15
61
62 Query Match 93.2%; Score 41; DB 4; Length 373;
63 Best Local Similarity 88.9%; Pred. No. 0.88;
64 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
65
66 QY 1 YGFSFTLAS 9
67
68 DB 246 YGFSFTLAS 254
69
70 RESULT 15

```

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Query Match      53.24; Score 4.; De 2; Length 387;
Best Local Similarity 89.54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

0y 1 FORSTIAS 9
24 257 VASSTIAS 275

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Search completed: September 24, 2003, 13:51:13  
Job time : 11.9213 secs























[illegible]





















```

RESULT 6
QWV1
AC QWV1
OCV1: PRELIMINARY: PRT: 352 AA
DI 01-NOV-1993 (TEMBREL: 12, Created)
DI 01-NOV-1993 (TEMBREL: 22, Last sequence update)
DI 01-NOV-1993 (TEMBREL: 23, Last annotation update)
DE Glycoprotein-39 (Fragment)
OS Salix nemoralis (Salix)
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Euteria: Rodentia: Sciurognathi: Muridae: Arctomys
OC NCB_TaxID:10126;
RN NCB TaxID:10126;
RN SEQUENCE FROM N.A.
NC STRAIN:Lexis;
PA Wessling U.; Boers A.P.M.; van Ruen K.;
RT potential autoantigen in arthritis
RL Submitted (Apr-1998) to the EMBL/GenBank/CCDB databases.
DR EMBL: AF075142; GenBank: AF075142; CCDB: AF075142;
DR InterPro: IPR01223; Glyco_Hydro_18;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR SMART: SM00436; Glyco_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
SQ SEQUENCE 352 AA: 35199 MW: CDS:9115263-9115263;
QWV1 Match 95.24; Score 43; EMBL 11; Length 352;
Best Local Similarity 88.94; Pref. NC: 1.7;
Matches 8; Conservative 1; Missed/Chg 0; Indels 0; Gaps 0;
DI 07 1 F08STLAS 9
DI 20 262 F08STLAS 270
RESULT 7
QWV1
AC QWV1
OCV1: PRELIMINARY: PRT: 347 AA
DI 01-MAR-2001 (TEMBREL: 15, Created)
DI 01-MAR-2001 (TEMBREL: 16, Last sequence update)
DI 01-MAR-2001 (TEMBREL: 23, Last annotation update)
DE Chitinotriaxinase precursor
OS Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Euteria: Primates: Catarrhini: Hominoidea: Homo.
RN NCB_TaxID:9606;
RN SEQUENCE FROM N.A.
NC STRAIN:Lexis;
PA Wessling U.; Boers A.P.M.; van Ruen K.;
RT potential autoantigen in arthritis
RL Submitted (Apr-1998) to the EMBL/GenBank/CCDB databases.
DR EMBL: AF075142; GenBank: AF075142; CCDB: AF075142;
DR InterPro: IPR01223; Glyco_Hydro_18;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR SMART: SM00436; Glyco_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
SQ SEQUENCE 352 AA: 35199 MW: CDS:9115263-9115263;
QWV1 Match 95.24; Score 43; EMBL 11; Length 352;
Best Local Similarity 88.94; Pref. NC: 1.7;
Matches 8; Conservative 1; Missed/Chg 0; Indels 0; Gaps 0;
DI 07 1 F08STLAS 9
DI 20 262 F08STLAS 270
RESULT 8
QWV1
AC QWV1
OCV1: PRELIMINARY: PRT: 347 AA
DI 01-MAR-2001 (TEMBREL: 15, Created)
DI 01-MAR-2001 (TEMBREL: 16, Last sequence update)
DI 01-MAR-2001 (TEMBREL: 23, Last annotation update)
DE Chitinotriaxinase precursor
OS Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Euteria: Primates: Catarrhini: Hominoidea: Homo.
RN NCB_TaxID:9606;
RN SEQUENCE FROM N.A.
NC STRAIN:Lexis;
PA Wessling U.; Boers A.P.M.; van Ruen K.;
RT potential autoantigen in arthritis
RL Submitted (Apr-1998) to the EMBL/GenBank/CCDB databases.
DR EMBL: AF075142; GenBank: AF075142; CCDB: AF075142;
DR InterPro: IPR01223; Glyco_Hydro_18;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR SMART: SM00436; Glyco_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
SQ SEQUENCE 352 AA: 35199 MW: CDS:9115263-9115263;
QWV1 Match 95.24; Score 43; EMBL 11; Length 352;
Best Local Similarity 88.94; Pref. NC: 1.7;
Matches 8; Conservative 1; Missed/Chg 0; Indels 0; Gaps 0;
DI 07 1 F08STLAS 9
DI 20 262 F08STLAS 270
RESULT 9
QWV1
AC QWV1
OCV1: PRELIMINARY: PRT: 349 AA
DI 01-MAR-2001 (TEMBREL: 23, Created)
DI 01-MAR-2001 (TEMBREL: 23, Last sequence update)
DI 01-MAR-2001 (TEMBREL: 23, Last annotation update)
DE Similar to chitinase 1-like 1
OS Mus musculus (Mouse)
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Euteria: Sciurognathi: Muridae: Arctomys: Mus.
RN NCB_TaxID:10090;
RN SEQUENCE FROM N.A.
NC STRAIN:Lexis;
PA Wessling U.; Boers A.P.M.; van Ruen K.;
RT potential autoantigen in arthritis
RL Submitted (Apr-2001) to the EMBL/GenBank/CCDB databases.
DR EMBL: AF075142; GenBank: AF075142; CCDB: AF075142;
DR InterPro: IPR01223; Glyco_Hydro_18;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR SMART: SM00436; Glyco_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
SQ SEQUENCE 381 AA: 42975 MW: EF588C; NCB_TaxID:10090;
QWV1 Match 95.24; Score 43; EMBL 11; Length 381;
Best Local Similarity 88.94; Pref. NC: 1.7;
Matches 8; Conservative 1; Missed/Chg 0; Indels 0; Gaps 0;
DI 07 1 F08STLAS 9
DI 20 262 F08STLAS 270
RESULT 10
QWV1
AC QWV1
OCV1: PRELIMINARY: PRT: 349 AA
DI 01-MAR-2001 (TEMBREL: 23, Created)
DI 01-MAR-2001 (TEMBREL: 23, Last sequence update)
DI 01-MAR-2001 (TEMBREL: 23, Last annotation update)
DE Similar to chitinase 1-like 1
OS Mus musculus (Mouse)
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Euteria: Sciurognathi: Muridae: Arctomys: Mus.
RN NCB_TaxID:10090;
RN SEQUENCE FROM N.A.
NC STRAIN:Lexis;
PA Wessling U.; Boers A.P.M.; van Ruen K.;
RT potential autoantigen in arthritis
RL Submitted (Apr-2001) to the EMBL/GenBank/CCDB databases.
DR EMBL: AF075142; GenBank: AF075142; CCDB: AF075142;
DR InterPro: IPR01223; Glyco_Hydro_18;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR Pfam: PF07074; Glyco_Hydro_18; 1;
DR SMART: SM00436; Glyco_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
DR NCBI: NC00477; Glyco_Hydro_18; 1;
SQ SEQUENCE 381 AA: 42975 MW: EF588C; NCB_TaxID:10090;
QWV1 Match 95.24; Score 43; EMBL 11; Length 381;
Best Local Similarity 88.94; Pref. NC: 1.7;
Matches 8; Conservative 1; Missed/Chg 0; Indels 0; Gaps 0;
DI 07 1 F08STLAS 9
DI 20 262 F08STLAS 270

```

NA The FANTOM Consortium.  
 NA Analysis of the mouse transcritpome based on functional annotation of  
 RL Nature 420:463-573(2002).  
 DR EMBL: AK01476; BAC3454.1; 9276645659239394 CCG4.  
 SQ SEQUENCE 387 AA; 4189 aa; 9276645659239394 CCG4.  
 Query Match 93.24; Score 41; DB 11; Length 356.  
 Best Local Similarity 86.94; Pred. No. 211.  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0.  
 QY 1 FORSFTLAS 9  
 DB 270 KRSFTLAS 276

RESUIT 10  
 AC Q05701 PRELIMINARY; PRT; 396 AA.  
 DT 01-JUN-2001 (TIMBLE); 17; Created.  
 DT 01-NOV-1996 (TIMBLE); 01; Last sequence update.  
 DT 01-MAR-2003 (TIMBLE); 23; Last annotation update.  
 DT 23-000021884k protein.  
 GN 23000021884k (mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 RN 131; LocusID:10556.  
 RP SEQUENCE FROM N.A. ...  
 RC MED:MF-10556; PubMed:1127551.  
 RA Kawai, J.; Shingawa, A.; Shibata, K.; Yoshino M.; Iton M.; Ishii Y.;  
 RA Arakawa, Y.; Kida, M.; Yamaguchi Y.; Kondo H.; Fukuda S.;  
 RA Saito T.; Ozaki Y.; Goshima T.; Sone H.; Kana-Kawa T.; Saito K.;  
 RA Kubota K.; Matsuda M.A.; Minamide K.; Matsuo S.; Casanova  
 RA Kuehl P.; Lewis S.; Matsui Y.; Nakano I.; Pradie G.; Quirk-McGough J.;  
 RA Schimi L.M.; Staudt F.; Szank R.; Tomita M.; Wozniak J.; Washio  
 RA Blake J.; Roffelli B.; Bouyana K.; Carrington M.; de Boerlan M.P.;  
 RA Brownstein K.J.; Bui C.; Fletcher C.; Fijita M.; Gariboldi K.;  
 RA Lironi, D.; Marthout D.; Mathias M.; Muzerelli, G.; Monaco P. H.;  
 RA Norberg P.; Atg B.; Ringwald M.; Rodigues J.; Sakamoto N.;  
 RA Sakai H.; Sato A.; Schoenbach C.; Seya S.; Shibata Y.; Storch K.P.;  
 RA Wyshak-Horiz A.; Yoshida K.; Hasegawa Y.; Kawai I. H.; Kotsuka S.;  
 RA Hayashizaki Y.; Jackson of a full-length mouse cDNA collection.  
 RL Nature 409:485-490(2001).  
 DR EMBL: AK090113; BAB3025.1; GenBank.  
 DR InterPro: IPR000477; 25; Gdb:Gdb:Gdb.  
 DR InterPro: IPR01221; Glyco\_hydro\_18.  
 DR InterPro: IPR001579; Glyco\_hydro\_18/2.  
 DR PRINTS: R00551; 25; Gdb:Gdb:Gdb.  
 DR Problem: R0000471; Glyco\_hydro\_18; 1.  
 DR PROSITE: PS01095; CHITINASE\_18; 1.  
 SQ SEQUENCE 396 AA; 4343 MW; 2286746547125 CPG4.  
 Query Match 93.24; Score 41; DB 11; Length 356.  
 Best Local Similarity 86.94; Pred. No. 211.  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0.  
 QY 1 FORSFTLAS 9  
 DB 267 KRSFTLAS 275

RESUIT 11  
 AC Q12311 PRELIMINARY; PRT; 466 AA.  
 DT 01-DEC-1996 (TIMBLE); 01; Created.  
 DT 01-NOV-1996 (TIMBLE); 01; Last sequence update.  
 DT 01-MAR-2003 (TIMBLE); 23; Last annotation update.  
 DT 23-000021884k protein.  
 GN 23000021884k (mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Carnivora; Canidae; Canis; Canis; Canis  
 RN 111; LocusID:10556.  
 RP SEQUENCE FROM N.A. PubMed:7523831.  
 RC MED:MF-10556; PubMed:7523831.  
 RA Scott R.G.; Renner G.R.; Str'lado A.; van Zonneveld A.J.; Aerts J.M.;  
 RA ...  
 RL Euk. Genes 270:222-26256(1995).  
 DR EMBL: C24515; AAC5246.1; ...  
 DR InterPro: IPR001579; Glyco\_hydro\_18.  
 DR InterPro: IPR01221; Glyco\_hydro\_18.  
 DR InterPro: IPR001579; Glyco\_hydro\_18/2.  
 DR PRINTS: R00551; 25; Gdb:Gdb:Gdb.  
 DR Problem: R0000471; Glyco\_hydro\_18; 1.  
 DR PROSITE: PS01095; CHITINASE\_18; 1.  
 SQ SEQUENCE 466 AA; 5189 MW; 5432012545350 CCG4.  
 Query Match 93.24; Score 41; DB 4; Length 466.  
 Best Local Similarity 86.94; Pred. No. 211.  
 Matches 6; Conservative 1; Mismatches 0; Gaps 0.  
 QY 1 FORSFTLAS 9  
 DB 267 KRSFTLAS 275

RESUIT 12  
 AC Q08514 PRELIMINARY; PRT; 265 AA.  
 DT 31-OCT-2002 (TIMBLE); 22; Created.  
 DT 31-OCT-2002 (TIMBLE); 22; Last sequence update.  
 DT 31-OCT-2003 (TIMBLE); 23; Last annotation update.  
 GN 438747P.  
 DR Q08514.  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Metazoa; Artiodactyla; Insecta; Psocoptera;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscoidomorpha;  
 CC Chiroptera; Chiroptera; Chiroptera; Chiroptera.  
 RN 111; LocusID:10556.  
 RP SEQUENCE FROM N.A.  
 RC MED:MF-10556; PubMed:7523831.  
 RA Stapleton M.; Brokstein P.; Hong L.; Adayani A.; Carlson J.;  
 RA Chang M.; Chavez C.; Dorsett V.; Dresek D.; Farfan C.; Frise S.;  
 RA Gao X.; Gao X.; Gao X.; Gao X.; Gao X.; Gao X.; Gao X.; Gao X.;  
 RA Patel S.; Phoummanong S.; Man K.; Yu C.; Lewis S.; Rubin G.M.;  
 RA O'Connell J.; ...  
 RN EMBL: AV118784; AAP05644.1; ...  
 DR FlyBase: FBgn004580; CG5157.  
 DR InterPro: IPR002597; CHITINASE\_18; 1.



[illegible]

PC TISSUE-Gut;  
 RA NSDLINE-98030543; PubMed=9360958;  
 RT Shu Z., Jacobs-Lorena M.,  
 RT Identification of a novel anti-specific chitinase gene from the  
 RT hemaphysalis vector acophelus sabiei.  
 RL J. Biol. Chem. 272:28995-28900(1997).  
 DR MEDLINE-98030543; PubMed=9360958;  
 DR InterPro: IPR001571; Glyco\_hydro\_18.  
 DR InterPro: IPR001571; Glyco\_hydro\_18.  
 DR InterPro: IPR001571; Glyco\_hydro\_18.  
 DR Pfam: PF02704; Glyco\_hydro\_18.  
 DR ProDom: PD000471; Glyco\_hydro\_18.  
 DR ProDom: PD000471; Glyco\_hydro\_18.  
 DR ProDom: PD000471; Glyco\_hydro\_18.  
 DR SMART: SM00536; Glyco\_18.  
 DR PROSITE: PS01295; CHITINASE\_18.  
 DR PROSITE: PS01295; CHITINASE\_18.  
 SW SWISSPROT: P00047; CHITINASE\_18.  
 SW SWISSPROT: P00047; CHITINASE\_18.

Query Match: 95.1% Score 18. -20.3; Length 525;  
 Identical Matches: 11

Matches: 7. Conservative 2. Mismatches 6. Indels 0. Gaps 0.

Qy 1 NUSTLAS 9

Db 279 NUSTLAS 287

Search completed: September 24, 2003, 13:47:21.  
 Job time: 3.2247 sec





80 Sequence 6 AA.  
 Query Match 100.0A; Score 42.9; Pos 21; Length 9;  
 Best Local Similarity 100.0A; Pos 0; Mismatches 0; Indels 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 0Y 1 FTLASSTG 9  
 1 FTLASSTG 9  
 Db 1 FTLASSTG 9  
 RESULT 4  
 AA020205  
 AA020205 standard; peptide: 1 AA.  
 AC AA020205:  
 DT 18-JUN-2002 (first entry)  
 XX Human cartilage glycoprotein (HC gp)-39 peptide (residues 263-273).  
 XX  
 XX Human cartilage glycoprotein-39; HC gp-39; autoimmune disorder; MMC;  
 XX Major histocompatibility complex; insulin-dependent diabetes mellitus;  
 XX Autoimmune disease; rheumatoid arthritis; myasthenia gravis; rheumatoid arthritis;  
 XX Immunoprotective; neuroprotective; therapy.  
 XX  
 XX Homo sapiens.  
 XX  
 XX MO200214870-A2.  
 XX  
 XX 21-FEB-2002.  
 XX  
 XX 08-AUG-2001; 2001WO-EP09116.  
 XX  
 XX 14-AUG-2000; 2000EP-G202844.  
 XX  
 XX (ALXU) A420 NOBEL NV.  
 XX  
 XX Steenbakkers PQA.  
 XX  
 XX WP1: 2002-269214/31.  
 XX  
 XX Method for diagnosing an autoimmune disease activity by detecting the  
 XX presence of an autoimmune peptide in a patient using antibodies specific against  
 XX (MMC)-peptide complex.  
 XX  
 XX Example 4; Page 23; 43pp; English.  
 XX  
 XX The patent discloses a method for diagnosing an autoimmune disease  
 XX activity. The method involves detecting the presence of an autoimmune  
 XX specific major histocompatibility complex (MMC)-peptide complex in a  
 XX patient suffering from an autoimmune disease with antibodies or its  
 XX presence. The method involves detecting the presence of an autoimmune  
 XX peptide. The method and antibodies are useful for diagnosing auto-  
 XX immune diseases or purifying autoimmune specific MMC-peptide complexes.  
 XX The method and antibodies are also useful in therapy for the treatment of  
 XX preparation for the treatment of autoimmune disorders such as insulin-  
 XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,  
 XX rheumatoid arthritis, myasthenia gravis, myasthenia gravis.  
 XX Human cartilage glycoprotein (HC gp)-39 peptide (residues 263-273). This  
 XX peptide is used in the exemplification of the invention.  
 XX  
 XX Sequence 11 AA:  
 0Y 1 FTLASSTG 9  
 3 FTLASSTG 9  
 Db 3 FTLASSTG 11

81 Sequence 11 AA.  
 Query Match 100.0A; Score 43.0; Pos 21; Length 11;  
 Best Local Similarity 100.0A; Pos 0; Mismatches 0; Indels 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;  
 0Y 1 FTLASSTG 9  
 3 FTLASSTG 9  
 Db 3 FTLASSTG 9  
 RESULT 6  
 AA020212  
 AA020212 standard; peptide: 11 AA.  
 AC AA020212:  
 DT 18-JUN-2002 (first entry)  
 XX Human cartilage glycoprotein (HC gp)-39 peptide (residues 264-274).  
 XX  
 XX Human cartilage glycoprotein (HC gp)-39 peptide (residues 264-274).  
 XX  
 XX Homo sapiens.  
 XX  
 XX MO200214870-A2.  
 XX  
 XX 21-FEB-2002.  
 XX  
 XX 08-AUG-2001; 2001WO-EP09116.  
 XX  
 XX 14-AUG-2000; 2000EP-G202844.  
 XX  
 XX (ALXU) A420 NOBEL NV.  
 XX  
 XX Steenbakkers PQA.  
 XX  
 XX WP1: 2002-269214/31.  
 XX  
 XX Method for diagnosing an autoimmune disease activity by detecting the  
 XX presence of an autoimmune peptide in a patient using antibodies specific against  
 XX (MMC)-peptide complex.  
 XX  
 XX Example 4; Page 23; 43pp; English.  
 XX  
 XX The patent discloses a method for diagnosing an autoimmune disease  
 XX activity. The method involves detecting the presence of an autoimmune  
 XX specific major histocompatibility complex (MMC)-peptide complex in a  
 XX patient suffering from an autoimmune disease with antibodies or its  
 XX presence. The method involves detecting the presence of an autoimmune  
 XX peptide. The method and antibodies are useful for diagnosing auto-  
 XX immune diseases or purifying autoimmune specific MMC-peptide complexes.  
 XX The method and antibodies are also useful in therapy for the treatment of  
 XX preparation for the treatment of autoimmune disorders such as insulin-  
 XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,  
 XX rheumatoid arthritis, myasthenia gravis, myasthenia gravis.  
 XX Human cartilage glycoprotein (HC gp)-39 peptide (residues 265-275). This  
 XX peptide is used in the exemplification of the invention.  
 XX  
 XX Sequence 11 AA:  
 0Y 1 FTLASSTG 9  
 3 FTLASSTG 9  
 Db 3 FTLASSTG 9









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DE      11111111
        3 FTASSETG 11
RESULT 13
ID      AAU03047
AC      AAU03047 standard; pep-23 AA.
XX      AAU03046:
XX      12-SEP-2003; (first entry)
XX      Human cartilage gp-39 autoimmune peptide #2.
DE      Human cartilage gp-39 autoimmune peptide #2.
XX      Human, autoimmune disease; epitope: antigen; rheumatoid arthritis.
XX      Immunosuppression.
XX      Homo sapiens.
OS      Synthetic.
XX      Key: Location/Qualifiers
XX      Modified-size 1
XX      Label= OTHER
XX      Note= "Other: desamino:111111"
XX      Modified-size 13
XX      Note= "Cysteine is oxidized"
XX      NC2000:2003 AA.
XX      26-APR-2001.
XX      12-OCT-2000; 200MOC-EP10230.
XX      15-OCT-1999; 58EP-0203427.
XX      (ALXU ) AKZO NOBEL NV.
XX      Van Stevenen CJ, Timmers CK, Van Galen EJM, Kuestel RWA, Boots AMH,
XX      Mittenberg MMH.
XX      NP1: 2001-367293/38.
XX      Modified peptide derived from human cartilage gp-39 protein epitope
XX      are useful in immunotherapy, especially in the treatment of arthritis.
XX      Claim 12; Page 39; 32pp; Engl-sh.
XX      The sequence represents a modified peptide derived from human cartilage
XX      gp-39 protein (see SEQ ID NO: 1) for use in immunotherapy.
XX      The peptides are useful for inducing tolerance induction in patients
XX      suffering from autoimmune diseases such as Rheumatoid arthritis.
XX      The peptides from the antigen-specific, non-toxic immunosuppression
XX      therapy as a very attractive alternative to non-specific
XX      immunosuppression..
XX      Sequence 13 AA:
XX      Query Match 100.0%; Score 43; FR 22; Length 13;
XX      Best Local Similarity 100.0%; Pred. No: 0.0083;
XX      Mismatches 0; Conservative 0; Mismatches 0; Gaps 0;
XX      QY 1 FTASSETG 9
XX      HZ 3 FTASSETG 11
XX      RESULT 14
XX      AAU03047
XX      AAU03047 standard; peptide: 13 AA.
XX      AAU03047:
XX      12-SEP-2003; (first entry)
XX      Human cartilage gp-39 autoimmune peptide #4.
XX      Human, autoimmune disease; epitope: antigen; rheumatoid arthritis;
XX      Immunosuppression.
XX      Homo sapiens.
OS      Synthetic.
XX      Key: Location/Qualifiers
XX      Modified-size 1

```

```

FT Modified-site 13 /note= "Connected to C61-(CH2CH3)3-OC(=O)-"
PI 13 /note= "C-terminus is acetylated"
PK K0200129081-M1.
XX 26-APR-2001.
XX 12-OCT-2000: 2000MO-EP10230.
XX 18-OCT-1999: 99EP-0203427.
XX (ALKD) AMCO ROBEL NV.
XX Van Skaveren CJ, Timmermans CM, Van Galen EJM, Kuntze PMW, Moos AMR;
PI Miltnerberg AM.
XX MPI: 2001-117253/36.
XX Modified peptides derived from human cartilage NP-70 protein epitope
PI are used in immunotherapy, especially in the treatment of arthritis
PC .
XX Claim 12, page 39, 32pp: English.
XX The sequence represents a modified peptide derived from human cartilage
CC NP-70 protein epitope and is used in immunotherapy.
XX The peptides are useful for inducing tolerance induction in patients
CC suffering from autoimmune diseases such as rheumatoid arthritis.
XX The peptides are also useful for inducing tolerance induction in patients
CC suffering from autoimmune diseases such as rheumatoid arthritis.
XX Thereby, a very attractive alternative to non-specific immunosuppression
CC immunosuppression.
XX Sequence 13 AA:
XX 150.00: Score 43, DB 22, Length 11;
Query Match Similarity 150.00: Score 43, DB 22, Length 11;
XX 91: Conservative 0, Identical 0, Matches 0; gaps 0.
XX 07 - PTLASSEP 9
XX 1111111
XX 06 3 PTLASSETC 11

```

Search completed: September 24, 2003, 13:41:20  
 Job time : 37.226 secs



CITY: Rockville  
STATE: Maryland  
COUNTRY: U.S.A.  
PRIORITY: 0  
COMPIER REASONABLE FURN:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Patent in Release #1.0, Version #1.2(EPO);  
CURRENT APPLICATION DATA: 08/06/1995  
FILING DATE: 25 MAR 1996  
CLASSIFICATION: 514  
REGISTRATION INFORMATION:  
NAME: Gortals, Mary Jo  
REGISTRATION NUMBER: 34,405  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-948-1144  
INFORMATION FOR SEQ ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid acids  
STRANDNESS: single  
SEQUENCE LENGTH: 11  
MOLECULE TYPE: peptide  
US-02-63-645-6  
US-02-63-645-6

Query Match 100.0% Score 41; IG 1; Length 13;  
Best Local Similarity 100.0%; Pired No. 0.629;  
Mismatch 5; Conservative 0; Mismatch 0; Indels 0; Gaps 0

1 FTLASSETG 9  
111111111  
1 FTLASSETG 11

REF: 1  
1 34-59+5  
2 Sequence 6: Application US/08634493  
3 Patent No. 584349  
4 APPLICANT: A.M.H. Boots  
5 APPLICANT: C.P.M. Verheijden  
6 ATTORNEY: N.V.S. Bos  
7 TITLE OF INVENTION: No. 584349c1: Peptides derived from autoantigen for use  
8 in the treatment of autoimmune diseases  
9 NUMBER OF SEQUENCES: 10  
10 ADDRESS: 1300 Piccard Drive, Suite 206  
11 STREET: 1300 Piccard Drive, Suite 206  
12 CITY: Rockville  
13 STATE: Maryland  
14 COUNTRY: USA  
15 2850  
16 COMPIER REASONABLE FURN:  
17 MEDIUM TYPE: Floppy disk  
18 COMPUTER: IBM PC compatible  
19 OPERATING SYSTEM: DOS  
20 SOFTWARE: Patent in Release #1.0, Version #1.25  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/28/634,493  
23 FILING DATE: 25-MAR-1996  
24 PRIOR APPLICATION DATA:  
25 APPLICATION NUMBER: US 38/619,545  
26 PRIORITY DATE: 27-OCT-1994  
27 APPLICATION NUMBER: PCT/EP95/0420  
28 FILING DATE: 25-OCT-1995  
29 APPLICATION NUMBER: NL 94031287  
30 PRIORITY DATE: 27-OCT-1994  
31 PRIOR APPLICATION DATA: NL 94031287

1 FILING DATE: 07-APR-1995  
 2 TELECOMMUNICATION INFORMATION:  
 3 TELEPHONE: (610) 675-2820  
 4 INFORMATION FOR SEQ ID NO: 6:  
 5 SEQUENCE CHARACTERISTICS:  
 6 TYPE: amino acid seqs  
 7 STRANDEDNESS: single  
 8 MOLECULE TYPE: polypeptide  
 9 US-06-634-491-6

Query Match: 100.0% Score 43; OW 3; Length 13;  
 Best Local Similarity: 100.0%; Pct. Id: 100.0%;  
 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

OT 1 FTASSTG 9  
 2D 3 FTASSTG 11

1 RESULT 9  
 2 Sequence 1: Application US/0940545  
 3 Patent No. 632020  
 4 APPLICANT: Stemmarketa PUA  
 5 TITLE OF INVENTION: Method of preparing a monoclonal  
 6 NUMBER OF SEQUENCES: antibody (as amended)  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Akzo No. 632020a1 Patent Dept.  
 9 CITY: Rockville  
 10 STATE: Maryland  
 11 ZIP: 20850

1 COMPUTER READABLE FORM:  
 2 MEDIUM TYPE: floppy disk  
 3 OPERATING SYSTEM: PC-DOS/MS-DOS  
 4 SOFTWARE: Patent In Release #1.0, Version #1.0 (EPO)  
 5 APPLICATION NUMBER: US/09/405,745

1 FILING DATE:  
 2 PRIOR APPLICATION DATA:  
 3 APPLICATION NUMBER: US/98/485,898  
 4 ATTORNEY/AGENT INFORMATION:  
 5 NAME: Sullivan, Michael G.  
 6 REGISTRATION NUMBER: 35,377  
 7 TELEPHONE: 301-948-7400  
 8 TELEFAX: 301-948-9751  
 9 INVENTOR CHARACTERISTICS: 1

1 LENGTH: 13 amino acids  
 2 TRANSDUCTION:  
 3 TOPOLOGY: linear dle  
 4 MOLECULE TYPE: protein  
 5 MOLECULE TYPE: Internal  
 6 US-06-634-491-6  
 7 Score 43; OW 3; Length 13;  
 8 Best Local Similarity: 100.0%; Pct. Id: 100.0%;  
 9 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

OT 1 FTASSTG 9  
 2D 3 FTASSTG 11

1 RESULT 6  
 2 Sequence 2: Application US/0940545  
 3 Patent No. 632020  
 4 APPLICANT: Stemmarketa PUA  
 5 TITLE OF INVENTION: Method of preparing a monoclonal  
 6 NUMBER OF SEQUENCES: antibody (as amended)  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Akzo No. 632020a1 Patent Dept.  
 9 CITY: Rockville  
 10 STATE: Maryland  
 11 ZIP: 20850

1 COMPUTER READABLE FORM:  
 2 MEDIUM TYPE: floppy disk  
 3 OPERATING SYSTEM: PC-DOS/MS-DOS  
 4 SOFTWARE: Patent In Release #1.0, Version #1.0 (EPO)  
 5 APPLICATION NUMBER: US/09/405,745

1 FILING DATE:  
 2 PRIOR APPLICATION DATA:  
 3 APPLICATION NUMBER: US/09/485,898  
 4 ATTORNEY/AGENT INFORMATION:  
 5 NAME: Sullivan, Michael G.  
 6 REGISTRATION NUMBER: 35,377  
 7 TELEPHONE: 301-948-7400  
 8 TELEFAX: 301-948-9751  
 9 INFORMATION FOR SEQ ID NO: 2

1 SEQUENCE CHARACTERISTICS: 1  
 2 LENGTH: 13 amino acids  
 3 TRANSDUCTION:  
 4 TOPOLOGY: linear  
 5 MOLECULE TYPE: protein  
 6 MOLECULE TYPE: Internal  
 7 US-06-634-491-6  
 8 Score 43; OW 3; Length 13;  
 9 Best Local Similarity: 100.0%; Pct. Id: 100.0%;  
 10 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 FILING DATE:  
 2 PRIOR APPLICATION DATA:  
 3 APPLICATION NUMBER: US/98/485,898  
 4 ATTORNEY/AGENT INFORMATION:  
 5 NAME: Sullivan, Michael G.  
 6 REGISTRATION NUMBER: 35,377  
 7 TELEPHONE: 301-948-7400  
 8 TELEFAX: 301-948-9751  
 9 INFORMATION FOR SEQ ID NO: 2

1 SEQUENCE CHARACTERISTICS: 1  
 2 LENGTH: 13 amino acids  
 3 TRANSDUCTION:  
 4 TOPOLOGY: linear  
 5 MOLECULE TYPE: protein  
 6 MOLECULE TYPE: Internal  
 7 US-06-634-491-6  
 8 Score 43; OW 3; Length 13;  
 9 Best Local Similarity: 100.0%; Pct. Id: 100.0%;  
 10 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

1 FILING DATE:  
 2 PRIOR APPLICATION DATA:  
 3 APPLICATION NUMBER: US/98/485,898  
 4 ATTORNEY/AGENT INFORMATION:  
 5 NAME: Sullivan, Michael G.  
 6 REGISTRATION NUMBER: 35,377  
 7 TELEPHONE: 301-948-7400  
 8 TELEFAX: 301-948-9751  
 9 INFORMATION FOR SEQ ID NO: 2

1 SEQUENCE CHARACTERISTICS: 1  
 2 LENGTH: 13 amino acids  
 3 TRANSDUCTION:  
 4 TOPOLOGY: linear  
 5 MOLECULE TYPE: protein  
 6 MOLECULE TYPE: Internal  
 7 US-06-634-491-6  
 8 Score 43; OW 3; Length 13;  
 9 Best Local Similarity: 100.0%; Pct. Id: 100.0%;  
 10 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

OT 1 FTASSTG 9  
 2D 3 FTASSTG 11



RESULT 12

TITLE OF INVENTION: Recombinant Ant-bodies for Human Therapy  
NUMBER OF SEQUENCES: 114







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1 STRANDNESS: single
2 TOPOLOGY: linear
3 MOLECULE TYPE: protein
4 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US 09-985-065-3
Query Match
100.0% Score 43; nb 10; Length 13:
Best Local Similarity 100.0%; Pred. No. 3; 2.8;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;
Oy 1 FTLASSTG 9
2b 1 FTLASSTG 11
RESULT 2
US 09-985-065-2
1 Sequence 2, Application US/09/95065
2 GENERAL INFORMATION:
3 APPLICANT: Stemblakers BSA
4 TITLE OF INVENTION: antibody (as amended)
5 NUMBER OF SEQUENCES: 3
6 CORRESPONDING AGENCIES: US Patent & Trademark Office
7 ADDRESS: 1300 Piccard Drive, Suite 204
8 CITY: Rockville
9 STATE: MD
10 COUNTRY: US
11 ZIP: 20850
12 MEDIUM TYPE: floppy disk
13 COMPUTER: IBM PC compatible
14 SOFTWARE: Patent Release 41.0, Version 41.30 (EPO)
15 CURRENT APPLICATION DATA: 09/09/05 065
16 APPLICATION NUMBER: US/99/95065
17 CLASSIFICATION: <unknown>
18 PRIOR APPLICATION DATA: 09/05/95 745
19 CORRESPONDING AGENCIES: US Patent & Trademark Office
20 ADDRESS: 1300 Piccard Drive, Suite 204
21 CITY: Rockville
22 STATE: MD
23 COUNTRY: US
24 ZIP: 20850
25 MEDIUM TYPE: floppy disk
26 COMPUTER: IBM PC compatible
27 SOFTWARE: Patent Release 41.0, Version 41.30 (EPO)
28 CURRENT APPLICATION DATA: 09/09/05 065
29 APPLICATION NUMBER: US/99/95065
30 CLASSIFICATION: <unknown>
31 PRIOR APPLICATION DATA: 09/05/95 745
32 CORRESPONDING AGENCIES: US Patent & Trademark Office
33 ADDRESS: 1300 Piccard Drive, Suite 204
34 CITY: Rockville
35 STATE: MD
36 COUNTRY: US
37 TELEPHONE: 301-448-9741
38 TELEFAX: 301-448-9741
39 INFORMATION FOR SEQ ID NO: 1:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 13;
42 TYPE: amino acid
43 STRANDNESS: single
44 MOLECULE TYPE: protein
45 FRAGMENT TYPE: internal
46 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-985-065-3
Query Match
100.0% Score 43; nb 10; Length 16:
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;
Oy 1 FTLASSTG 9
2b 4 FTLASSTG 12
RESULT 4
US 09-985-065-2
1 Sequence 36, Application US/09/91943
2 GENERAL INFORMATION:
3 APPLICANT: Stemblakers BSA
4 TITLE OF INVENTION: antibody (as amended)
5 NUMBER OF SEQUENCES: 3
6 CORRESPONDING AGENCIES: US Patent & Trademark Office
7 ADDRESS: 1300 Piccard Drive, Suite 204
8 CITY: Rockville
9 STATE: MD
10 COUNTRY: US
11 ZIP: 20850
12 MEDIUM TYPE: floppy disk
13 COMPUTER: IBM PC compatible
14 SOFTWARE: Patent Release 41.0, Version 41.30 (EPO)
15 CURRENT APPLICATION DATA: 09/09/05 837
16 APPLICATION NUMBER: US 60/791,274
17 CLASSIFICATION: <unknown>
18 PRIOR APPLICATION DATA: 09/05/95 249
19 CORRESPONDING AGENCIES: US Patent & Trademark Office
20 ADDRESS: 1300 Piccard Drive, Suite 204
21 CITY: Rockville
22 STATE: MD
23 COUNTRY: US
24 ZIP: 20850
25 MEDIUM TYPE: floppy disk
26 COMPUTER: IBM PC compatible
27 SOFTWARE: Patent Ver. 2.1

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1 SEQUENCE NO. US2002041150A1
2 GENERAL INFORMATION:
3 APPLICANT: Stemblakers BSA
4 TITLE OF INVENTION: antibody (as amended)
5 NUMBER OF SEQUENCES: 3
6 CORRESPONDING AGENCIES: US Patent & Trademark Office
7 ADDRESS: 1300 Piccard Drive, Suite 204
8 CITY: Rockville
9 STATE: MD
10 COUNTRY: US
11 ZIP: 20850
12 MEDIUM TYPE: floppy disk
13 COMPUTER: IBM PC compatible
14 SOFTWARE: Patent Release 41.0, Version 41.30 (EPO)
15 CURRENT APPLICATION DATA: 09/09/05 065
16 APPLICATION NUMBER: US/99/95065
17 CLASSIFICATION: <unknown>
18 PRIOR APPLICATION DATA: 09/05/95 745
19 CORRESPONDING AGENCIES: US Patent & Trademark Office
20 ADDRESS: 1300 Piccard Drive, Suite 204
21 CITY: Rockville
22 STATE: MD
23 COUNTRY: US
24 ZIP: 20850
25 MEDIUM TYPE: floppy disk
26 COMPUTER: IBM PC compatible
27 SOFTWARE: Patent Release 41.0, Version 41.30 (EPO)
28 CURRENT APPLICATION DATA: 09/09/05 065
29 APPLICATION NUMBER: US/99/95065
30 CLASSIFICATION: <unknown>
31 PRIOR APPLICATION DATA: 09/05/95 745
32 CORRESPONDING AGENCIES: US Patent & Trademark Office
33 ADDRESS: 1300 Piccard Drive, Suite 204
34 CITY: Rockville
35 STATE: MD
36 COUNTRY: US
37 TELEPHONE: 301-448-9741
38 TELEFAX: 301-448-9741
39 INFORMATION FOR SEQ ID NO: 1:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 13;
42 TYPE: amino acid
43 STRANDNESS: single
44 MOLECULE TYPE: protein
45 FRAGMENT TYPE: internal
46 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-985-065-3
Query Match
100.0% Score 43; nb 10; Length 16:
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;
Oy 1 FTLASSTG 9
2b 4 FTLASSTG 12
RESULT 4
US 09-985-065-2
1 Sequence 36, Application US/09/91943
2 GENERAL INFORMATION:
3 APPLICANT: Stemblakers BSA
4 TITLE OF INVENTION: antibody (as amended)
5 NUMBER OF SEQUENCES: 3
6 CORRESPONDING AGENCIES: US Patent & Trademark Office
7 ADDRESS: 1300 Piccard Drive, Suite 204
8 CITY: Rockville
9 STATE: MD
10 COUNTRY: US
11 ZIP: 20850
12 MEDIUM TYPE: floppy disk
13 COMPUTER: IBM PC compatible
14 SOFTWARE: Patent Release 41.0, Version 41.30 (EPO)
15 CURRENT APPLICATION DATA: 09/09/05 837
16 APPLICATION NUMBER: US 60/791,274
17 CLASSIFICATION: <unknown>
18 PRIOR APPLICATION DATA: 09/05/95 249
19 CORRESPONDING AGENCIES: US Patent & Trademark Office
20 ADDRESS: 1300 Piccard Drive, Suite 204
21 CITY: Rockville
22 STATE: MD
23 COUNTRY: US
24 ZIP: 20850
25 MEDIUM TYPE: floppy disk
26 COMPUTER: IBM PC compatible
27 SOFTWARE: Patent Ver. 2.1

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1 SEQ ID NO: 56
2 LENGTH: 199
3 TYPE: PAT
4 FEATURE: Artificial Sequence
5 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
6 US-09-815-837-56
7
8 Query Match
9 Score: 43, Dm: 9, Length: 199
10 Best Local Similarity: 100.0%, Ident: 0, Mismatches: 0, Indels: 0, Gaps: 0
11 Matches: 0
12
13 07 1 FTLASSETG 9
14 11111111
15 8 FTLASSETG 16
16
17 RESULT 5
18 US-09-815-837-56
19 Sequence 56, Application US/09815837
20 Patent No. US2002008241A1
21 GENERAL INFORMATION: Darriek
22 APPLICANT: Zhu, Shirley
23 APPLICANT: Atcill, Subashini
24 APPLICANT: Corixa Corporation
25 TITLE OF INVENTION: Immune Modulators and Related Methods
26 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
27 CURRENT FILING DATE: 2001-03-22
28 PRIOR APPLICATION NUMBER: US 60/191,274
29 PRIOR FILING DATE: 2000-05-15
30 PRIOR APPLICATION NUMBER: US 60/204,249
31 PRIOR FILING DATE: 2000-05-15
32 PRIOR FILING DATE: 2001-01-23
33 NUMBER OF SEQ ID NOS: 129
34 SEQ ID NO: 60
35 TYPE: PAT
36 FEATURE: Artificial Sequence
37 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
38 US-09-815-837-60
39
40 Query Match
41 Score: 43, Dm: 9, Length: 199
42 Best Local Similarity: 100.0%, Ident: 0, Mismatches: 0, Indels: 0, Gaps: 0
43 Matches: 0
44
45 07 1 FTLASSETG 9
46 11111111
47 8 FTLASSETG 15
48
49 RESULT 6
50 US-09-815-837-40
51 Sequence 102, Application US/09815837
52 Patent No. US2002008241A1
53 GENERAL INFORMATION: Darriek
54 APPLICANT: Zhu, Shirley
55 APPLICANT: Atcill, Subashini
56 APPLICANT: Corixa Corporation
57 TITLE OF INVENTION: Immune Modulators and Related Methods
58 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
59 CURRENT FILING DATE: 2001-03-22
60 PRIOR APPLICATION NUMBER: US 60/191,274
61 PRIOR FILING DATE: 2000-05-15
62 PRIOR APPLICATION NUMBER: US 60/204,249
63 PRIOR FILING DATE: 2001-01-23
64 NUMBER OF SEQ ID NOS: 129
65 SEQ ID NO: 60
66 TYPE: PAT
67 FEATURE: Artificial Sequence
68 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
69 US-09-815-837-40
70
71 Query Match
72 Score: 43, Dm: 9, Length: 209
73 Best Local Similarity: 100.0%, Ident: 0, Mismatches: 0, Indels: 0, Gaps: 0
74 Matches: 0
75
76 07 1 FTLASSETG 9
77 11111111
78 7 FTLASSETG 15
79
80 RESULT 7
81 US-09-815-837-58
82 Sequence 58, Application US/09815837
83 Patent No. US2002008241A1
84 GENERAL INFORMATION: Darriek
85 APPLICANT: Zhu, Shirley
86 APPLICANT: Atcill, Subashini
87 APPLICANT: Corixa Corporation
88 TITLE OF INVENTION: Immune Modulators and Related Methods
89 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
90 CURRENT FILING DATE: 2001-03-22
91 PRIOR APPLICATION NUMBER: US 60/191,274
92 PRIOR FILING DATE: 2000-05-15
93 PRIOR APPLICATION NUMBER: US 60/204,249
94 PRIOR FILING DATE: 2001-01-23
95 NUMBER OF SEQ ID NOS: 129
96 SEQ ID NO: 38
97 TYPE: PAT
98 FEATURE: Artificial Sequence
99 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
100 US-09-815-837-58
101
102 Query Match
103 Score: 43, Dm: 9, Length: 209
104 Best Local Similarity: 100.0%, Ident: 0, Mismatches: 0, Indels: 0, Gaps: 0
105 Matches: 0
106
107 07 1 FTLASSETG 9
108 11111111
109 7 FTLASSETG 15
110
111 RESULT 8
112 US-09-815-837-40
113 Sequence 40, Application US/09815837
114 Patent No. US2002008241A1
115 GENERAL INFORMATION: Darriek
116 APPLICANT: Zhu, Shirley
117 APPLICANT: Atcill, Subashini
118 APPLICANT: Corixa Corporation
119 TITLE OF INVENTION: Immune Modulators and Related Methods
120 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
121 CURRENT FILING DATE: 2001-03-22
122 PRIOR APPLICATION NUMBER: US 60/191,274
123 PRIOR FILING DATE: 2000-05-15
124 PRIOR APPLICATION NUMBER: US 60/204,249
125 PRIOR FILING DATE: 2001-01-23
126 NUMBER OF SEQ ID NOS: 129
127 SEQ ID NO: 38
128 TYPE: PAT
129 FEATURE: Artificial Sequence
130 OTHER INFORMATION: Description of Artificial Sequence: C524-A1 single
131 US-09-815-837-40
132

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Best Local Similarity: 100.0%; Seed: 43; M: 5; Length: 212;  
Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q: 1 P1ASSETG 9  
DB: 8 P1ASSETG 16

RESULT 12  
US-09-815-837-41  
1 Sequence 41, Application US/09415837  
2 Patent No. US200208441A1  
3 GENERAL INFORMATION: Description of Artificial Sequence:CO597 single  
4 TITLE OF INVENTION: Chain recombinant MIC class II molecule  
5 APPLICANT: Zymo, Shirley  
6 APPLICANT: Zymo, Shirley  
7 APPLICANT: Armitall, Subhashini  
8 APPLICANT: Corixa Corporation  
9 TITLE OF INVENTION: Immune Modulators and Related Methods  
10 FILE REFERENCE: US-05-08-0703 US/05/08-0703  
11 CURRENT FILING DATE: 2001-03-22  
12 PRIOR APPLICATION NUMBER: US 60/191,271  
13 PRIOR FILING DATE: 2000-05-15  
14 PRIOR APPLICATION NUMBER: US 60/204,249  
15 PRIOR FILING DATE: 2000-05-15  
16 NUMBER OF SEQ ID NOS: 129  
17 SOFTWARE: Patent Ver. 2.1  
18 LENGTH: 212  
19 TYPE: PRT  
20 OTHER INFORMATION: Description of Artificial Sequence:CO597 single  
21 FEATURE:  
22 US-09-815-837-41  
Query Match  
1 Best Local Similarity: 100.0%; Seed: 43; M: 5; Length: 212;  
2 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q: 1 P1ASSETG 9  
DB: 8 P1ASSETG 16

RESULT 13  
US-09-815-837-41  
1 Sequence 41, Application US/09415837  
2 Patent No. US200208441A1  
3 GENERAL INFORMATION: Description of Artificial Sequence:CO598 single  
4 TITLE OF INVENTION: Chain recombinant MIC class II molecule  
5 APPLICANT: Zymo, Shirley  
6 APPLICANT: Zymo, Shirley  
7 APPLICANT: Armitall, Subhashini  
8 APPLICANT: Corixa Corporation  
9 TITLE OF INVENTION: Immune Modulators and Related Methods  
10 FILE REFERENCE: US-05-08-0703 US/05/08-0703  
11 CURRENT FILING DATE: 2001-03-22  
12 PRIOR APPLICATION NUMBER: US 60/191,271  
13 PRIOR FILING DATE: 2000-05-15  
14 PRIOR APPLICATION NUMBER: US 60/204,249  
15 PRIOR FILING DATE: 2000-05-15  
16 NUMBER OF SEQ ID NOS: 129  
17 SOFTWARE: Patent Ver. 2.1  
18 LENGTH: 212  
19 TYPE: PRT  
20 OTHER INFORMATION: Description of Artificial Sequence:CO598 single  
21 FEATURE:  
22 US-09-815-837-43  
Query Match  
1 Best Local Similarity: 100.0%; Seed: 43; M: 5; Length: 212;  
2 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q: 1 P1ASSETG 9  
DB: 8 P1ASSETG 16

RESULT 14  
US-09-815-837-41  
1 Sequence 41, Application US/09415837  
2 Patent No. US200208441A1  
3 GENERAL INFORMATION: Description of Artificial Sequence:CO599 single  
4 TITLE OF INVENTION: Chain recombinant MIC class II molecule  
5 APPLICANT: Zymo, Shirley  
6 APPLICANT: Zymo, Shirley  
7 APPLICANT: Armitall, Subhashini  
8 APPLICANT: Corixa Corporation  
9 TITLE OF INVENTION: Immune Modulators and Related Methods  
10 FILE REFERENCE: US-05-08-0703 US/05/08-0703  
11 CURRENT FILING DATE: 2001-03-22  
12 PRIOR APPLICATION NUMBER: US 60/191,271  
13 PRIOR FILING DATE: 2000-05-15  
14 PRIOR APPLICATION NUMBER: US 60/204,249  
15 PRIOR FILING DATE: 2000-05-15  
16 NUMBER OF SEQ ID NOS: 129  
17 SOFTWARE: Patent Ver. 2.1  
18 LENGTH: 212  
19 TYPE: PRT  
20 OTHER INFORMATION: Description of Artificial Sequence:CO599 single  
21 FEATURE:  
22 US-09-815-837-43  
Query Match  
1 Best Local Similarity: 100.0%; Seed: 43; M: 5; Length: 212;  
2 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q: 1 P1ASSETG 9  
DB: 8 P1ASSETG 16

RESULT 15  
US-09-815-837-41  
1 Sequence 41, Application US/09415837  
2 Patent No. US200208441A1  
3 GENERAL INFORMATION: Description of Artificial Sequence:CO600 single  
4 TITLE OF INVENTION: Chain recombinant MIC class II molecule  
5 APPLICANT: Zymo, Shirley  
6 APPLICANT: Zymo, Shirley  
7 APPLICANT: Armitall, Subhashini  
8 APPLICANT: Corixa Corporation  
9 TITLE OF INVENTION: Immune Modulators and Related Methods  
10 FILE REFERENCE: US-05-08-0703 US/05/08-0703  
11 CURRENT FILING DATE: 2001-03-22  
12 PRIOR APPLICATION NUMBER: US 60/191,271  
13 PRIOR FILING DATE: 2000-05-15  
14 PRIOR APPLICATION NUMBER: US 60/204,249  
15 PRIOR FILING DATE: 2000-05-15  
16 NUMBER OF SEQ ID NOS: 129  
17 SOFTWARE: Patent Ver. 2.1  
18 LENGTH: 212  
19 TYPE: PRT  
20 OTHER INFORMATION: Description of Artificial Sequence:CO600 single  
21 FEATURE:  
22 US-09-815-837-43  
Query Match  
1 Best Local Similarity: 100.0%; Seed: 43; M: 5; Length: 212;  
2 Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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1 PRIOR APPLICATION NUMBER: US 50/264,093
2
3 PRIOR FILING DATE: 2001-01-23
4
5 NUMBER OF SEQ. ID NOS: 129
6
7 NUMBER OF SEQ. ID NOS: 129
8 SEQ ID NO 44
9
10 SEQ ID NO 44
11
12 LENGTH: 223
13
14 TYPE: PRT
15
16 SOURCE: Artificial Sequence
17
18 FEATURE
19
20 OTHER INFORMATION: Description of Artificial Sequence: Coding
21
22 OTHER INFORMATION: Chain coordinates: NC Class II molecule
23
24 US-09-815,897-44
25
26 Query Match 100.00; Score 43; len 7; Length 211;
27 Query Local Similarity: 100.00; Pos 1;
28 Matches: 2; conservative: 0; Mismatches: 0; Gaps: 0;
29
30 QY 1 FTASSETG 9
31
32 DB 8 FTASSETG 16
33
34 Search completed: September 24, 2003, 14:29:36
35
36 Seq Time: 24.1216 secs

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C:Accession: F51325  
 A:Gene: vnt  
 C:Species: unassigned ATP-binding cassette proteins; ATP-binding cassette family  
 Query Match 86.0%; Score 77; DB 2; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 332 FTLASSET 159

RESULT 3  
 S51327  
 A:Description: *Escherichia coli* (strain ATCC 8739) *glnK* gene, complete cds.  
 C:Accession: F51327  
 A:Gene: glnK  
 C:Species: *Escherichia coli* (strain ATCC 8739)  
 Query Match 76.7%; Score 71; DB 2; Length 183;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 265 FTLASSET 272

RESULT 4  
 C59046  
 A:Description: conserved hypothetical protein NRC135 - Methanobacterium thermautotrophicum (strain pyro) (strain ATCC 35062) *glnK* gene, complete cds.  
 C:Accession: C59046  
 A:Gene: glnK  
 C:Species: *Methanobacterium thermautotrophicum* (strain pyro) (strain ATCC 35062)  
 Query Match 76.7%; Score 71; DB 2; Length 183;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 265 FTLASSET 272

RESULT 5  
 C59046  
 A:Description: conserved hypothetical protein NRC135 - Methanobacterium thermautotrophicum (strain pyro) (strain ATCC 35062) *glnK* gene, complete cds.  
 C:Accession: C59046  
 A:Gene: glnK  
 C:Species: *Methanobacterium thermautotrophicum* (strain pyro) (strain ATCC 35062)  
 Query Match 76.7%; Score 71; DB 2; Length 183;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 265 FTLASSET 272

C:Accession: F51325  
 A:Gene: vnt  
 C:Species: unassigned ATP-binding cassette proteins; ATP-binding cassette family  
 Query Match 86.0%; Score 77; DB 2; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 332 FTLASSET 159

RESULT 3  
 S51327  
 A:Description: *Escherichia coli* (strain ATCC 8739) *glnK* gene, complete cds.  
 C:Accession: F51327  
 A:Gene: glnK  
 C:Species: *Escherichia coli* (strain ATCC 8739)  
 Query Match 76.7%; Score 71; DB 2; Length 183;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 265 FTLASSET 272

RESULT 4  
 C59046  
 A:Description: conserved hypothetical protein NRC135 - Methanobacterium thermautotrophicum (strain pyro) (strain ATCC 35062) *glnK* gene, complete cds.  
 C:Accession: C59046  
 A:Gene: glnK  
 C:Species: *Methanobacterium thermautotrophicum* (strain pyro) (strain ATCC 35062)  
 Query Match 76.7%; Score 71; DB 2; Length 183;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 265 FTLASSET 272

RESULT 5  
 C59046  
 A:Description: conserved hypothetical protein NRC135 - Methanobacterium thermautotrophicum (strain pyro) (strain ATCC 35062) *glnK* gene, complete cds.  
 C:Accession: C59046  
 A:Gene: glnK  
 C:Species: *Methanobacterium thermautotrophicum* (strain pyro) (strain ATCC 35062)  
 Query Match 76.7%; Score 71; DB 2; Length 183;  
 Best Local Similarity 87.5%; Pred. No. 27;  
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLASSET 1  
 Db 265 FTLASSET 272





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Query Match: 72.18; Score 31; DB 2; Length: 202;
Best Local Similarity: 72.18; Score 31; DB 2; Length: 202;
Mismatches: 0; Mismatches: 0; Gaps: 0;

Cy 1 F1ASSTG 9
DB 141 F1ASSTG 149

RESULT 12
T2068
C:Species: Cnemidophorus elegans
C:Accession: T2068
C:Date: 15-Oct-1995
C:SequenceRevision: 15-Oct-1995
C:Submitted to the EMBL Data Library: December 1995
A:Reference number: 219213
A:Accession: T2068
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Length: 202
A:Experimental source: clone C5184
A:Cross-references: EMBL:268215; FIDN:CA92454.1; GSPDB:GN00022; CESP:C5184.6
C:Genetic: C5184.6
A:Map position: 4
A:Introns: 35/2; 9/3; 144/3; 200/3; 251/2

Query Match: 72.18; Score 31; DB 2; Length: 318;
Best Local Similarity: 77.98; Freq No: 47;
Mismatches: 7; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

Cy 1 F1ASSTG 9
DB 133 F1ASSTG 14;

RESULT 13
T24905
C:Species: Cnemidophorus elegans
C:Accession: T24905
C:Date: 15-Oct-1995
C:SequenceRevision: 15-Oct-1995
C:Submitted to the EMBL Data Library: Apr. 1994
A:Reference number: 219522
A:Accession: T24905
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Length: 318
A:Experimental source: clone T14C1
A:Cross-references: EMBL:270437; FIDN:CA3446.6; GSPDB:GN00026; CESP:T24905
C:Genetic: T14C1
A:Map position: 1
A:Introns: 17/3; 141/2; 289/1; 254/2

Query Match: 72.18; Score 31; DB 2; Length: 320;
Best Local Similarity: 72.18; Score 31; DB 2; Length: 320;
Mismatches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;

Cy 1 F1ASSTG 9
DB 10 F1ASSTG 18

RESULT 14
T2068
C:Species: Cnemidophorus elegans
C:Accession: T2068
C:Date: 15-Oct-1995
C:SequenceRevision: 15-Oct-1995
C:Submitted to the EMBL Data Library: December 1995
A:Reference number: 219213
A:Accession: T2068
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Length: 202
A:Experimental source: clone C5184
A:Cross-references: EMBL:268215; FIDN:CA92454.1; GSPDB:GN00022; CESP:T2068
C:Genetic: C5184.6
A:Map position: 4
A:Introns: 35/2; 9/3; 144/3; 200/3; 251/2

Query Match: 72.18; Score 31; DB 2; Length: 324;
Best Local Similarity: 72.18; Score 31; DB 2; Length: 324;
Mismatches: 6; Conservative: 1; Mismatches: 1; Indels: 0; Gaps: 0;

Cy 2 F1ASSTG 9
DB 215 F1ASSTG 242

RESULT 15
T24905
C:Species: Cnemidophorus elegans (strain PA01)
C:Accession: T24905
C:Date: 15-Sep-2000
C:SequenceRevision: 15-Sep-2000
C:Submitted to the EMBL Data Library: Sep. 2000
A:Reference number: A82550
A:Accession: T24905
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Length: 324
A:Experimental source: strain PA01
A:Cross-references: EMBL:1047377; FIDN:1598404
C:Genetic: A82550
A:Map position: 1
A:Introns: 35/2; 9/3; 144/3; 200/3; 251/2

Query Match: 72.18; Score 31; DB 2; Length: 373;
Best Local Similarity: 72.18; Score 31; DB 2; Length: 373;
Mismatches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;

Cy 1 F1ASSTG 9
DB 140 F1ASSTG 146

Search completed: September 24, 2003, 13:49:18
Job time: 11:52:13 secs

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[illegible][illegible]













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OY 1 FLASSTG 8
DB 265 FLASSTG 72

RESULT 10
OY 09207 PRELIMINARY PRT: 1265 AA
AC 09207:
DT 01-OCT-2002 (TFMSBcel: 22, Created)
DT 01-MAR-2003 (TFMSBcel: 23, Last sequence update)
DE Hypothetical protein KXALING (Fragment)
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eumammalia; Primates; Catarrhini; Hominoidea; Hominidae;
CC Homininae; Homo
RN [1]
RP SEQUENCE FROM M.A.
RX MEDLINE:1018126; P:BMJ3-10718159;
RA Nagase T., Kikuno K., Ishikawa K., Hirotsugu M., Chate C., Kawanishi Y.,
RA Kato T., Nakamura Y., Nakamura K., Nakamura K., Nakamura K., Nakamura K.,
RT for large proteins in vitro.
DB ENR: J090707; J090707; J090707
DR InterPro: IPR003347; PFJ00000
DR SMART: SM00258; TSC_1
KW Hypothetical protein.
SQ SEQUENCE 1265 AA: 141291 MW: 330450.534 DQ54:

Query Match
Best Local Similarity 76.7% Score 33; DB 4: Length 1265;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0.

OY 2 FLASSTG 9
DB 183 FLASSTG 90

RESULT 11
OY 09300 PRELIMINARY PRT: 212 AA
AC 09300:
DT 01-OCT-2002 (TFMSBcel: 22, Created)
DT 01-MAR-2003 (TFMSBcel: 23, Last sequence update)
DE Hypothetical protein (fragment)
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eumammalia; Primates; Catarrhini; Hominidae; Homininae;
CC Homininae; Homo
RN [1]
RP SEQUENCE FROM M.A.
RX Medline:1018126; P:BMJ3-10718159;
RA Stenwall B., Kawanishi Y., Kawanishi Y., Kawanishi Y., Kawanishi Y.,
RA Stenwall B., Kawanishi Y., Kawanishi Y., Kawanishi Y., Kawanishi Y.,
RT for large proteins in vitro.
DB ENR: J090707; J090707; J090707
DR InterPro: IPR003347; PFJ00000
DR SMART: SM00258; TSC_1
KW Hypothetical protein.
SQ SEQUENCE 212 AA: 240377 MW: 89656.16845 DQ54:

Query Match
Best Local Similarity 87.5% Score 33; DB 4: Length 2162;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

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OY 2 FLASSTG 9
DB 183 FLASSTG 1066

RESULT 12
OY 09307 PRELIMINARY PRT: 231 AA
AC 09307:
DT 01-OCT-2002 (TFMSBcel: 22, Created)
DT 01-MAR-2003 (TFMSBcel: 23, Last sequence update)
DE Hypothetical protein KXALING (Fragment)
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eumammalia; Primates; Catarrhini; Hominidae; Homininae;
CC Homininae; Homo
RN [1]
RP SEQUENCE FROM M.A.
RX MEDLINE:1018126; P:BMJ3-10718159;
RA Nagase T., Kikuno K., Ishikawa K., Hirotsugu M., Chate C., Kawanishi Y.,
RA Kato T., Nakamura Y., Nakamura K., Nakamura K., Nakamura K., Nakamura K.,
RT for large proteins in vitro.
DB ENR: J090707; J090707; J090707
DR InterPro: IPR003347; PFJ00000
DR SMART: SM00258; TSC_1
KW Hypothetical protein.
SQ SEQUENCE 231 AA: 28923 MW: 51685.71454 DQ54:

Query Match
Best Local Similarity 66.7% Score 33; DB 4: Length 231;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

OY 1 FLASSTG 5
DB 7 FLASSTG 25

RESULT 13
OY 09308 PRELIMINARY PRT: 241 AA
AC 09308:
DT 01-MAR-2003 (TFMSBcel: 23, Created)
DT 01-MAR-2003 (TFMSBcel: 23, Last sequence update)
DE Hypothetical protein KXALING (Fragment)
OS Homo sapiens (Human)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eumammalia; Primates; Catarrhini; Hominidae; Homininae;
CC Homininae; Homo
RN [1]
RP SEQUENCE FROM M.A.
RX MEDLINE:1018126; P:BMJ3-10718159;
RA Nagase T., Kikuno K., Ishikawa K., Hirotsugu M., Chate C., Kawanishi Y.,
RA Kato T., Nakamura Y., Nakamura K., Nakamura K., Nakamura K., Nakamura K.,
RT for large proteins in vitro.
DB ENR: J090707; J090707; J090707
DR InterPro: IPR003347; PFJ00000
DR SMART: SM00258; TSC_1
KW Hypothetical protein.
SQ SEQUENCE 241 AA: 28923 MW: 51685.71454 DQ54:

Query Match
Best Local Similarity 66.7% Score 33; DB 4: Length 231;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0.

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```

RA HALLACK D.G., INDOLSKA Z.G., KREBS K.F., ANGERLIN C.W., DALL H.,
RA ALAN M., FRELICH T., HOU S., DALLA S.C., JENNIS P.P., QUNT A.D.,
RA SCHARD S., LOWE T.M., LIANG P., RILEY M., BLOOD L., DASSARNA S.,
RA PRIC N.H.I. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AC00079; MAG12976.1.
DR InterPro: PR00337; M08C_N.
DR Pfam: PF0413; M08C_1.
DR Conserved Domains: M08C_N.1.
KW Complete Proteome: M08C_N.1.
SQ SEQUENCE 261 AA; 3527 MW; 6F510A69778769 CHECK;
Query Match 74.4% Score 32, DB 17, Length 261;
Best Local Similarity 56.7% Freq. No. 79;
Matches 6; Conservative 1; Mismatches 2; Index 0; Gaps 0;
Q7 1 FTASSEQ 5
ED 37 15463535 46
RESULT 14
OSMVL PRELIMINARY: PRT. 352 AA.
AC OSMVL-1995 (TREMUR). 1; Created.
AC OSMVL-1995 (TREMUR). 22; Last sequence update.
DT 01-MAR-2001 (TREMUR). 23; Last annotation update.
DR EMBL: AC00079; MAG12976.1.
DR InterPro: PR00337; M08C_N.
DR Pfam: PF0413; M08C_1.
DR Conserved Domains: M08C_N.1.
KW Complete Proteome: M08C_N.1.
SQ SEQUENCE 261 AA; 3527 MW; 6F510A69778769 CHECK;
Query Match 74.4% Score 32, DB 17, Length 261;
Best Local Similarity 56.7% Freq. No. 79;
Matches 6; Conservative 1; Mismatches 2; Index 0; Gaps 0;
Q7 1 FTASSEQ 5
ED 37 15463535 46
RESULT 14
OSMVL PRELIMINARY: PRT. 352 AA.
AC OSMVL-1995 (TREMUR). 1; Created.
AC OSMVL-1995 (TREMUR). 22; Last sequence update.
DT 01-MAR-2001 (TREMUR). 23; Last annotation update.
DR EMBL: AC00079; MAG12976.1.
DR InterPro: PR00337; M08C_N.
DR Pfam: PF0413; M08C_1.
DR Conserved Domains: M08C_N.1.
KW Complete Proteome: M08C_N.1.
SQ SEQUENCE 261 AA; 3527 MW; 6F510A69778769 CHECK;
Query Match 74.4% Score 32, DB 17, Length 261;
Best Local Similarity 56.7% Freq. No. 79;
Matches 6; Conservative 1; Mismatches 2; Index 0; Gaps 0;
Q7 1 FTASSEQ 5
ED 37 15463535 46

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OC Cyprinidae: Danio.
RA HALLACK D.G., INDOLSKA Z.G., KREBS K.F., ANGERLIN C.W., DALL H.,
RA ALAN M., FRELICH T., HOU S., DALLA S.C., JENNIS P.P., QUNT A.D.,
RA SCHARD S., LOWE T.M., LIANG P., RILEY M., BLOOD L., DASSARNA S.,
RA PRIC N.H.I. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AC00079; MAG12976.1.
DR InterPro: PR00337; M08C_N.
DR Pfam: PF0413; M08C_1.
DR Conserved Domains: M08C_N.1.
KW Complete Proteome: M08C_N.1.
SQ SEQUENCE 261 AA; 3527 MW; 6F510A69778769 CHECK;
Query Match 74.4% Score 32, DB 17, Length 261;
Best Local Similarity 56.7% Freq. No. 79;
Matches 6; Conservative 1; Mismatches 2; Index 0; Gaps 0;
Q7 1 FTASSEQ 5
ED 37 15463535 46

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Job time : 10:2247 sec

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GenScan version 5.1.1  
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 Run on: September 24, 2003, 13:35:23, Search time: 0.9133 seconds  
 14 867 Million cell updates/sec  
 Title: US-09-744-282-3  
 Sequence: 1 YDOESVKS 9  
 Scoring table: BIOSIM62  
 Searched: Gap0 10.0, Gapset 0.5  
 328717 seqs, 42310238 residues  
 Total number of hits satisfying chosen parameters: 328717  
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 Maximum DB seq length: 230005760  
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 and is divided by and 1% of the total score distribution.

## SUMMARY

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1	45	105.0	9	1	US-08-625-542-3	Sequence 1, Appl.
2	46	100.0	2	2	US-08-634-493-1	Sequence 1, Appl.
3	46	100.0	1	3	US-08-634-493-1	Sequence 1, Appl.
4	46	100.0	1	4	US-08-634-493-1	Sequence 1, Appl.
5	46	100.0	1	5	US-09-127-702-31	Sequence 51, Appl.
6	46	100.0	1	6	US-09-127-702-31	Sequence 51, Appl.
7	43	93.5	38	4	US-09-439-1460-7	Sequence 177, Appl.
8	33	71.7	11.5	4	US-09-114-003-3226	Sequence 223, Ap
9	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
10	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
11	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
12	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
13	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
14	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
15	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
16	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
17	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
18	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
19	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
20	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
21	32	69.6	468	1	US-08-204-5508-4	Sequence 2, Appl.
22	31	67.4	371	4	US-08-551-524-2	Sequence 39, Appl.
23	31	67.4	371	4	US-08-551-524-2	Sequence 39, Appl.
24	31	67.4	371	4	US-08-551-524-2	Sequence 39, Appl.
25	30	65.2	181	4	US-09-114-003-3226	Sequence 187, A
26	30	65.2	181	4	US-09-114-003-3226	Sequence 187, A
27	30	65.2	181	4	US-09-114-003-3226	Sequence 187, A
28	30	65.2	181	4	US-09-114-003-3226	Sequence 187, A
29	30	65.2	181	4	US-09-114-003-3226	Sequence 187, A
30	30	65.2	181	4	US-09-114-003-3226	Sequence 187, A

28 30 65.2 244 4 US-09-328-352-4316  
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 45 30 65.2 449 1 US-08-074-121-6

## ALIGNMENTS

Sequence 1: 61-61-3  
 Patent No. 5736007  
 APPLICANT: BOEBS, Anna M.H.  
 APPLICANT: Invention, Gilbertus F.M.  
 TITLE OF INVENTION: device for use in immunotherapy of autoimmune diseases derived from  
 TITLE OF INVENTION: device for use in immunotherapy of autoimmune diseases derived from  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Anzo No. 5736007; Patent Department  
 STATE: Maryland  
 CITY: Rockville  
 ZIP: 20850-5100  
 COMPUTER READABLE FORM  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA: Issue #1.0, Version #1.0 (EPO)  
 APPLICATION NUMBER: US/09/610,645  
 CLASSIFICATION: 511  
 ATTORNEY/AGENT INFORMATION:  
 TELECOMMUNICATIONS NUMBER: 34,409  
 TELECOMMUNICATIONS INFORMATION:  
 TELEPHONE: 100-947-4433  
 TELEFAX: 100-947-4433  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 STANDEX: single  
 WEIGHT: 100.00  
 US-08-619-644-3

Query Match 100.0% Score 449, DB 1, Length 9;  
 Best Local Similarity 100.0% Pred. No. 2 (e-05)  
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;  
 1 YDOESVKS 9  
 1 YDOESVKS 9





1 FILING DATE: 07-APR-1995  
 2 TELEPHONE: (301) 598-5300  
 3 TELEFAX: (301) 577-0847  
 4 INVENTOR: JAMES M. FROST, JR.  
 5 SEQUENCE CHARACTERISTICS: 7  
 6 LENGTH: 15 amino acids  
 7 STRANDEDNESS: single  
 8 TOPOLOGY: linear  
 9 NATURE OF TYPE: peptide  
 10 US-08-614,414.7

Query Match: Similarity: 100.0%, Score 45; ID: 2; Length: 15;  
 Mismatches: 0; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 YDQGSYS 5  
 ID 3 YDQGSYS 11

RESULT 5  
 US-09-171-705-51

1 Sequence 51, Application US/0911705  
 2 Patent No. 6184234  
 3 APPLICANT: VERTEC, ANNA M.H.  
 4 APPLICANT ADDRESS: ANNA M.H.  
 5 APPLICANT VERIFICATION: GILBERTUS F. K.  
 6 TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTI-CD4 SPECIFIC  
 7 FILE REFERENCE: 0/96154 US  
 8 CURRENT APPLICATION NUMBER: US/0911705  
 9 PRIOR FILING DATE: 1995-02-09  
 10 NUMBER OF SEQ ID NOS: 18  
 11 SOFTWARE: Patent Ver. 2.0  
 12 LENGTH: 16  
 13 TYPE: PPT  
 14 NATURE: Artificial Sequence

Query Match: Similarity: 100.0%, Score 45; ID: 3; Length: 15;  
 Mismatches: 0; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 YDQGSYS 5  
 ID 3 YDQGSYS 15

RESULT 6  
 US-09-171-705-52

1 Sequence 52, Application US/0911705  
 2 Patent No. 6184234  
 3 APPLICANT: VERTEC, ANNA M.H.  
 4 APPLICANT ADDRESS: ANNA M.H.  
 5 APPLICANT VERIFICATION: GILBERTUS F. K.  
 6 TITLE OF INVENTION: IMMUNOSUPPRESSIVE PEPTIDE  
 7 FILE REFERENCE: 0/96154 US  
 8 CURRENT APPLICATION NUMBER: US/0911705  
 9 PRIOR FILING DATE: 1995-02-09  
 10 NUMBER OF SEQ ID NOS: 18  
 11 SOFTWARE: Patent Ver. 2.0  
 12 LENGTH: 16  
 13 TYPE: PPT  
 14 NATURE: Artificial Sequence

Query Match: Similarity: 100.0%, Score 45; ID: 4; Length: 15;  
 Mismatches: 0; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 YDQGSYS 5  
 ID 3 YDQGSYS 15

1 OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM  
 US-09-171-705-52

Query Match: Similarity: 100.0%, Score 46; ID: 1; Length: 15;  
 Mismatches: 0; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 YDQGSYS 9  
 ID 1 YDQGSYS 9

RESULT 7  
 US-09-171-705-53

1 Sequence 17, Application US/9459740  
 2 Patent No. 6464975  
 3 APPLICANT: VERTEC, ALBERT J. T.  
 4 TITLE OF INVENTION: Compositions and Methods for Altering Cell Migration  
 5 FILE REFERENCE: 0/94,016A US/09/459,740  
 6 CURRENT FILING DATE: 1995-12-15  
 7 PRIOR APPLICATION NUMBER: 60/711,456  
 8 NUMBER OF SEQ ID NOS: 11  
 9 SOFTWARE: Patent Ver. 2.1  
 10 LENGTH: 16  
 11 TYPE: PPT  
 12 NATURE: Artificial Sequence

Query Match: Similarity: 88.5%, Score 43; ID: 4; Length: 16;  
 Mismatches: 8; Conservative: 17; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 YDQGSYS 9  
 ID 339 YDQGSYS 316

RESULT 8  
 US-09-171-705-54

1 Sequence 54, Application US/9459740  
 2 Patent No. 6464975  
 3 APPLICANT: VERTEC, ALBERT J. T.  
 4 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
 5 FILE REFERENCE: 0/94,016A US/09/459,740  
 6 CURRENT APPLICATION NUMBER: US/94/597,402  
 7 PRIOR FILING DATE: 1997-11-08  
 8 NUMBER OF SEQ ID NOS: 60/955,779  
 9 SOFTWARE: Patent Ver. 2.1  
 10 LENGTH: 116  
 11 TYPE: PPT  
 12 NATURE: Staphylococcus epidermidis

Query Match: Similarity: 62.7%, Score 33; ID: 4; Length: 119;  
 Mismatches: 5; Conservative: 31; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 YDQGSYS 8  
 ID 109 YDQGSYS 116

RESULT 5 (us-09-592)  
 1 Sequence 5292, Application US/09134002C  
 2 Patent No. 6360370  
 3 APPLICANT: EVANT BIOLOGICALS-STAMM ET AL  
 4 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATES TO STAPHYLOCOCCUS  
 5 FILE REFERENCE: GPC-07 IDENTIFIS FOR DIAGNOSTICS AND THERAPEUTIC  
 6 CURRENT APPLICATION NUMBER: 05/09/134,002C  
 7 PRIORITY FILING DATE: 05/09/134,002C  
 8 PRIORITY FILING DATE: 05/09/134,002C  
 9 PRIORITY FILING DATE: 05/09/134,002C  
 10 PRIORITY FILING DATE: 05/09/134,002C  
 11 PRIORITY FILING DATE: 05/09/134,002C  
 12 PRIORITY FILING DATE: 05/09/134,002C  
 13 PRIORITY FILING DATE: 05/09/134,002C  
 14 PRIORITY FILING DATE: 05/09/134,002C  
 15 PRIORITY FILING DATE: 05/09/134,002C  
 16 PRIORITY FILING DATE: 05/09/134,002C  
 17 PRIORITY FILING DATE: 05/09/134,002C  
 18 PRIORITY FILING DATE: 05/09/134,002C  
 19 PRIORITY FILING DATE: 05/09/134,002C  
 20 PRIORITY FILING DATE: 05/09/134,002C  
 21 PRIORITY FILING DATE: 05/09/134,002C  
 22 PRIORITY FILING DATE: 05/09/134,002C  
 23 PRIORITY FILING DATE: 05/09/134,002C  
 24 PRIORITY FILING DATE: 05/09/134,002C  
 25 PRIORITY FILING DATE: 05/09/134,002C  
 26 PRIORITY FILING DATE: 05/09/134,002C  
 27 PRIORITY FILING DATE: 05/09/134,002C  
 28 PRIORITY FILING DATE: 05/09/134,002C  
 29 PRIORITY FILING DATE: 05/09/134,002C  
 30 PRIORITY FILING DATE: 05/09/134,002C  
 31 PRIORITY FILING DATE: 05/09/134,002C  
 32 PRIORITY FILING DATE: 05/09/134,002C  
 33 PRIORITY FILING DATE: 05/09/134,002C  
 34 PRIORITY FILING DATE: 05/09/134,002C  
 35 PRIORITY FILING DATE: 05/09/134,002C  
 36 PRIORITY FILING DATE: 05/09/134,002C  
 37 PRIORITY FILING DATE: 05/09/134,002C  
 38 PRIORITY FILING DATE: 05/09/134,002C  
 39 PRIORITY FILING DATE: 05/09/134,002C  
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 42 PRIORITY FILING DATE: 05/09/134,002C  
 43 PRIORITY FILING DATE: 05/09/134,002C  
 44 PRIORITY FILING DATE: 05/09/134,002C  
 45 PRIORITY FILING DATE: 05/09/134,002C  
 46 PRIORITY FILING DATE: 05/09/134,002C  
 47 PRIORITY FILING DATE: 05/09/134,002C  
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 54 PRIORITY FILING DATE: 05/09/134,002C  
 55 PRIORITY FILING DATE: 05/09/134,002C  
 56 PRIORITY FILING DATE: 05/09/134,002C  
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 58 PRIORITY FILING DATE: 05/09/134,002C  
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 64 PRIORITY FILING DATE: 05/09/134,002C  
 65 PRIORITY FILING DATE: 05/09/134,002C  
 66 PRIORITY FILING DATE: 05/09/134,002C  
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 69 PRIORITY FILING DATE: 05/09/134,002C  
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 71 PRIORITY FILING DATE: 05/09/134,002C  
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 83 PRIORITY FILING DATE: 05/09/134,002C  
 84 PRIORITY FILING DATE: 05/09/134,002C  
 85 PRIORITY FILING DATE: 05/09/134,002C  
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 87 PRIORITY FILING DATE: 05/09/134,002C  
 88 PRIORITY FILING DATE: 05/09/134,002C  
 89 PRIORITY FILING DATE: 05/09/134,002C  
 90 PRIORITY FILING DATE: 05/09/134,002C  
 91 PRIORITY FILING DATE: 05/09/134,002C  
 92 PRIORITY FILING DATE: 05/09/134,002C  
 93 PRIORITY FILING DATE: 05/09/134,002C  
 94 PRIORITY FILING DATE: 05/09/134,002C  
 95 PRIORITY FILING DATE: 05/09/134,002C  
 96 PRIORITY FILING DATE: 05/09/134,002C  
 97 PRIORITY FILING DATE: 05/09/134,002C  
 98 PRIORITY FILING DATE: 05/09/134,002C  
 99 PRIORITY FILING DATE: 05/09/134,002C  
 100 PRIORITY FILING DATE: 05/09/134,002C

RESULT 11 (us-08-204-558-2)  
 1 MOLECULE TYPE: PROTEIN  
 2 Query Match  
 3 Best Local Similarity: 66.7%  
 4 Matches: 6, Conservative: 1, Mismatches: 2, Indels: 0, Gaps: 0  
 5 J 100SEQS 5  
 6 CH 155 Y200A00NS 164  
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1 APPLICANT: MYAEL, Sachio  
 2 APPLICANT: MYAEL, Sachio  
 3 TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,  
 4 TITLE OF INVENTION: Variant Gene Of The Buryne And Method For Producing  
 5 NUMBER OF SEQUENCES: 14  
 6 CORRESPONDENCE ADDRESS: 1400 Westchester Road, Suite 500 East  
 7 STREET: 810 Gatehouse Road, Suite 500 East  
 8 CITY: Falls Church  
 9 STATE: Virginia  
 10 COUNTRY: U.S.A.  
 11 ZIP: 22042  
 12 COMPUTER READABLE FORM:  
 13 MEDIUM TYPE: floppy disk  
 14 OPERATING SYSTEM: PC-DOS/MS-DOS  
 15 CURRENT APPLICATION DATA: 1.0, Version 41.30  
 16 APPLICATION NUMBER: US/09/204,656B  
 17 CLASSIFICATION: 435  
 18 ATTORNEY/AGENT INFORMATION:  
 19 REF: 32181  
 20 REF: 234-222P  
 21 TELEPHONE: (703) 205-8640  
 22 TELEFAX: (703) 205-8640  
 23 INFORMATION FOR SEQ. ID NO. 6:  
 24 SEQUENCE CHARACTERISTICS:  
 25 LENGTH: 458 amino acids  
 26 TOPOLOGY: 1 linear  
 27 MOLECULE TYPE: protein  
 28 US-09-204-656B-9

Query Match 69.61; Score 32; DB 1; Length 458;  
 Boot Loc. Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 4; Gaps 0.

QY 1 YUOESKYS 9  
 DB 156 YUOANOVUS 164

RESULT 13  
 US-08-204-666B-8  
 1 GENERAL INFORMATION: US/05/1465A  
 2 Patent No. 551582  
 3 APPLICANT: Ishikawa, Kazuhiko  
 4 APPLICANT: Miyai, Sachio  
 5 APPLICANT: Miyai, Sachio  
 6 TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,  
 7 TITLE OF INVENTION: Variant Gene Of The Buryne And Method For Producing  
 8 NUMBER OF SEQUENCES: 14  
 9 CORRESPONDENCE ADDRESS: 1400 Westchester Road, Suite 500 East  
 10 STREET: 810 Gatehouse Road, Suite 500 East  
 11 CITY: Falls Church  
 12 STATE: Virginia  
 13 COUNTRY: U.S.A.  
 14 ZIP: 22042  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: floppy disk  
 17 OPERATING SYSTEM: PC-DOS/MS-DOS  
 18 CURRENT APPLICATION DATA: 1.0, Version 41.30  
 19 APPLICATION NUMBER: US/09/204,656B  
 20 CLASSIFICATION: 435  
 21 ATTORNEY/AGENT INFORMATION:  
 22 REF: 32181  
 23 REF: 234-222P  
 24 TELEPHONE: (703) 205-8600  
 25 TELEFAX: (703) 205-8650  
 26 INFORMATION FOR SEQ ID NO: 6:  
 27 SEQUENCE CHARACTERISTICS:  
 28 LENGTH: 458 amino acids  
 29 TOPOLOGY: 1 linear  
 30 MOLECULE TYPE: protein  
 31 US-09-204-656B-9

APPLICATION NUMBER: US/08/204,604B  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 REF: 32181  
 REF: 234-222P  
 TELEPHONE: (703) 205-8600  
 TELEFAX: (703) 205-8650  
 INFORMATION FOR SEQ. ID NO. 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 458 amino acids  
 TOPOLOGY: 1 linear  
 MOLECULE TYPE: protein  
 US-08-204-656B-8

Query Match 69.64; Score 32; DB 1; Length 458;  
 Boot Loc. Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 2; Gaps 0.

QY 1 YUOESKYS 9  
 DB 156 YUOANOVUS 164

RESULT 13  
 US-08-204-6722-6  
 1 GENERAL INFORMATION: US/04/7072  
 2 Patent No. 4611449  
 3 APPLICANT: Miyai, Sachio  
 4 APPLICANT: Miyai, Sachio  
 5 APPLICANT: Miyai, Sachio  
 6 TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,  
 7 TITLE OF INVENTION: Variant Gene Of The Buryne And Method For Producing  
 8 NUMBER OF SEQUENCES: 14  
 9 CORRESPONDENCE ADDRESS: 1400 Westchester Road, Suite 500 East  
 10 STREET: 810 Gatehouse Road, Suite 500 East  
 11 CITY: Falls Church  
 12 STATE: Virginia  
 13 COUNTRY: U.S.A.  
 14 ZIP: 22042  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: floppy disk  
 17 OPERATING SYSTEM: PC-DOS/MS-DOS  
 18 CURRENT APPLICATION DATA: 1.0, Version 41.25  
 19 APPLICATION NUMBER: US/08/470,702  
 20 CLASSIFICATION: 435  
 21 ATTORNEY/AGENT INFORMATION:  
 22 REF: 32181  
 23 REF: 234-222P  
 24 TELEPHONE: (703) 205-8600  
 25 TELEFAX: (703) 205-8650  
 26 INFORMATION FOR SEQ ID NO: 6:  
 27 SEQUENCE CHARACTERISTICS:  
 28 LENGTH: 458 amino acids  
 29 TOPOLOGY: 1 linear  
 30 MOLECULE TYPE: protein  
 31 US-08-204-656B-8

Query Match 69.64; Score 32; DB 1; Length 458;  
 Boot Loc. Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 1; Mismatches 2; Gaps 0.

QY 1 YUOESKYS 9  
 DB 156 YUOANOVUS 164

RESULT 13  
 US-08-204-6722-6  
 1 GENERAL INFORMATION: US/04/7072  
 2 Patent No. 4611449  
 3 APPLICANT: Miyai, Sachio  
 4 APPLICANT: Miyai, Sachio  
 5 APPLICANT: Miyai, Sachio  
 6 TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,  
 7 TITLE OF INVENTION: Variant Gene Of The Buryne And Method For Producing  
 8 NUMBER OF SEQUENCES: 14  
 9 CORRESPONDENCE ADDRESS: 1400 Westchester Road, Suite 500 East  
 10 STREET: 810 Gatehouse Road, Suite 500 East  
 11 CITY: Falls Church  
 12 STATE: Virginia  
 13 COUNTRY: U.S.A.  
 14 ZIP: 22042  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: floppy disk  
 17 OPERATING SYSTEM: PC-DOS/MS-DOS  
 18 CURRENT APPLICATION DATA: 1.0, Version 41.25  
 19 APPLICATION NUMBER: US/08/470,702  
 20 CLASSIFICATION: 435  
 21 ATTORNEY/AGENT INFORMATION:  
 22 REF: 32181  
 23 REF: 234-222P  
 24 TELEPHONE: (703) 205-8600  
 25 TELEFAX: (703) 205-8650  
 26 INFORMATION FOR SEQ ID NO: 6:  
 27 SEQUENCE CHARACTERISTICS:  
 28 LENGTH: 458 amino acids  
 29 TOPOLOGY: 1 linear  
 30 MOLECULE TYPE: protein  
 31 US-08-204-656B-8

1 TOPOLOGY: linear  
2 MOLECULE TYPE: Protein  
3 HYPOTHEICAL: NO  
4 ANTI-SENSE: NO  
US-09-744-282-3

Query Match 65.61, Score 32, DB 1, Length 668  
Query Match 65.61, Score 32, DB 1, Length 668  
Matches 6: Conservative 2, Mismatches 2, Gaps 0

QY 1 YGGDSKVS 9  
1111 111  
DB 156 YGGDAQVDS 164

RESULT 15  
1 Sequence 7, Application US/8847702  
2 Patent No. 531145  
3 GENERAL INFORMATION  
4 APPLICANT: WATSON, FRU  
5 APPLICANT: ISHIKAWA, KAZUHIKO  
6 APPLICANT: ISHIMIZU, SHIRO  
7 APPLICANT: KAWA, KAZUHIKO  
8 TITLE OF INVENTION: VARIANT TYPE CARBOHYDRATE HYDROLASE  
9 TITLE OF INVENTION: VARIANT TYPE OF THE ENZYME AND METHOD FOR PRODUCING  
10 NUMBER OF SEQUENCES: 2  
11 CORRESPONDENCE ADDRESS: 1-1-1, Nishi-Shinjyuku, Shinjyuku-ku, Tokyo 163-8602, Japan  
12 STREET: 2110 Calhoun Road, Suite 502, East  
13 CITY: Falls Church  
14 STATE: Virginia  
15 COUNTRY: U.S.A.  
16 ZIP: 22042  
17 COMPUTER: IBM PC compatible  
18 PERIOD TYPE: EASY disk  
19 SOFTWARE: IBM PC compatible  
20 SOFTWARE: IBM PC compatible  
21 SOFTWARE: IBM PC compatible  
22 CURRENT APPLICATION DATA  
23 APPLICATION NUMBER: US/8847702  
24 APPLICATION NUMBER: US/8847702  
25 CLASSIFICATION: 433  
26 PRIORITY APPLICATION DATA: US 09/204,656  
27 FILING DATE: 02-MAR-1994  
28 ATTORNEY/AGENT INFORMATION:  
29 REGISTRATION NUMBER: 32,181  
30 REFERENCE/DOC NUMBER: 234-252P  
31 TELEPHONE: (703) 205-6000  
32 TELEFAX: (703) 205-6000  
33 INFORMATION FOR SEQ ID NO: 7:  
34 SEQUENCE CHARACTERISTICS:  
35 TYPE: amino acids  
36 STRANDEDNESS: single  
37 MOLECULE TYPE: protein  
38 HYPOTHEICAL: NO  
39 ANTI-SENSE: NO  
US-09-744-282-3

Query Match 65.61, Score 32, DB 1, Length 668  
Query Match 65.61, Score 32, DB 1, Length 668  
Matches 6: Conservative 2, Mismatches 2, Gaps 0

QY 1 YGGDSKVS 9  
1111 111  
DB 156 YGGDAQVDS 164

Search completed: September 24, 2003, 13:51:14  
Job time: 11.9213 secs





















## Citations:

C Keywords: glycosyltransferase; hexamethyltransferase

Query Match: 75.0% Score: 16.0 (10/2) Length: 441  
 Best Local Similarity: 75.0%  
 Matches: 5, Conservative: 1, Mismatches: 0, Gaps: 0,

QY 1 YDQ6SV 6  
 1 1 1 1 1 1  
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Accession: S59569

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OR protein - protein search, using sw model

Run on: September 24, 2003, 13:14:08 - Search time: 11.775 seconds

79,250 Million cell updates/sec

Title: US-09-744-282-5

Percent score: 55

Sequence: 1: FGGSGSTLASSL 11

Scoring table: SLOSI0M2

Gap: 10.0 - reward: 0.5

Searched: 283372 seqs, 9635660 residues

Total number of hits satisfying chosen parameters: 46130

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listed: 1151 45 summaries

Database:

1: p1r-76-\*

2: p1r-2-\*

3: p1r-3-\*

4: p1r-4-\*

Prod No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the whole search distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	65	100	6	2	cat-10p-lyc-2
2	62	75	4	2	cat-10p-lyc-2
3	62	75	4	2	cat-10p-lyc-2
4	45	69	2	2	cat-10p-lyc-2
5	41	63	1	2	cat-10p-lyc-2
6	41	63	1	2	cat-10p-lyc-2
7	40	61	1	2	cat-10p-lyc-2
8	40	61	1	2	cat-10p-lyc-2
9	39	60	1	2	cat-10p-lyc-2
10	39	60	1	2	cat-10p-lyc-2
11	39	60	1	2	cat-10p-lyc-2
12	39	60	1	2	cat-10p-lyc-2
13	39	60	1	2	cat-10p-lyc-2
14	37	56	2	2	cat-10p-lyc-2
15	37	56	2	2	cat-10p-lyc-2
16	37	56	2	2	cat-10p-lyc-2
17	37	56	2	2	cat-10p-lyc-2
18	37	56	2	2	cat-10p-lyc-2
19	37	56	2	2	cat-10p-lyc-2
20	36	55	4	2	cat-10p-lyc-2
21	36	55	4	2	cat-10p-lyc-2
22	36	55	4	2	cat-10p-lyc-2
23	36	55	4	2	cat-10p-lyc-2
24	36	55	4	2	cat-10p-lyc-2
25	36	55	4	2	cat-10p-lyc-2
26	35	53	8	2	cat-10p-lyc-2
27	35	53	8	2	cat-10p-lyc-2
28	35	53	8	2	cat-10p-lyc-2

30 35 53 8 187 2 S5411  
 31 35 53 8 187 2 R8174  
 32 35 53 8 187 2 A7560  
 33 35 53 8 187 2 A7560  
 34 35 53 8 187 2 A7560  
 35 35 53 8 187 2 A7560  
 36 35 53 8 187 2 A7560  
 37 35 53 8 187 2 A7560  
 38 35 53 8 187 2 A7560  
 39 35 53 8 187 2 A7560  
 40 35 53 8 187 2 A7560  
 41 35 53 8 187 2 A7560  
 42 35 53 8 187 2 A7560  
 43 35 53 8 187 2 A7560  
 44 35 53 8 187 2 A7560  
 45 35 53 8 187 2 A7560

## ALIGNMENTS

45627 :  
 cat10p-lyc-2  
 1: cat10p-lyc-2  
 2: cat10p-lyc-2  
 3: cat10p-lyc-2  
 4: cat10p-lyc-2  
 5: cat10p-lyc-2  
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 27: cat10p-lyc-2  
 28: cat10p-lyc-2

30 35 53 8 187 2 S5411  
 31 35 53 8 187 2 R8174  
 32 35 53 8 187 2 A7560  
 33 35 53 8 187 2 A7560  
 34 35 53 8 187 2 A7560  
 35 35 53 8 187 2 A7560  
 36 35 53 8 187 2 A7560  
 37 35 53 8 187 2 A7560  
 38 35 53 8 187 2 A7560  
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 40 35 53 8 187 2 A7560  
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 42 35 53 8 187 2 A7560  
 43 35 53 8 187 2 A7560  
 44 35 53 8 187 2 A7560  
 45 35 53 8 187 2 A7560

PIRN12500, B.M. *INRA* data library, November 1995  
 A:Accession: S61550  
 A:Residues: 1-145; 17-217-330; 330-330; WWW:JALBOVSKY@COMPEFFL@INRA.FR  
 A:Cross-references: EMBL:U081015; KID:q108503; PIRN:CA61603.1; E:q108506  
 C:Dates: 10-Jun-1998 *sequence\_revision* 10-Jun-1998 *text\_change* 21-Jul-2000  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 A:Gene: btp19 *Streptomyces olivaceus* strain 410  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/40/Product: breast-tissue protein btp19 status predicted *CMAT*  
 Query Match 95.4% Score 62; db 2; Length 403;  
 Best Local Similarity 92.1%; Pred. No. 3,0045;  
 Matches 22; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPROSPTLASS 13  
 DB 260 PPROSPTLASS 272

RESULT 7  
 S51127  
 heparin-binding glycoprotein 18k (btp19) [btp19]  
 C:Accession: S51127; Gene: B.M. Waller; January 1995  
 C:Dates: 19-Mar-1997 *sequence\_revision* 15-Mar-1997 *text\_change* 22-2-2004  
 C:Keywords: submitted to the EMBL Data Library  
 A:Description: Identification of a 33kDa heparin-binding glycoprotein (btp19) in *Dictyostelium*  
 A:Accession: S51127  
 A:Status: Preliminary  
 A:Molecule type: RNA  
 A:Cross-references: EMBL:U081015; KID:q108503; PIRN:CA61603.1; PTD:3614598  
 C:Dates: 10-Jun-1998 *sequence\_revision* 10-Jun-1998 *text\_change* 21-Jul-2000  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 A:Gene: btp19 *Streptomyces olivaceus* strain 410  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/40/Product: breast-tissue protein btp19 status predicted *CMAT*  
 Query Match 91.8%; Score 62; db 2; Length 481;  
 Best Local Similarity 92.3%; Pred. No. 3,0045;  
 Matches 12; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPROSPTLASS 13  
 DB 255 PPROSPTLASS 271

RESULT 4  
 T4445  
 chitinase (EC 3.2.1.14) [imported] - African malaria mosquito  
 C:Accession: T4445; Gene: B.M. Waller; January 1995  
 C:Dates: 21-Jan-2000 *sequence\_revision* 21-Jan-2000 *text\_change* 21-Jan-2000  
 C:Keywords: submitted to the EMBL Data Library  
 A:Description: Chitinase from *Anopheles gambiae* (strain 9P) submitted to the EMBL Data Library, June 1997  
 A:Reference number: 22277  
 A:Accession: T4445  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Cross-references: EMBL:U081015; KID:q108503; PIRN:CA61603.1  
 C:Dates: 10-Jun-1998 *sequence\_revision* 10-Jun-1998 *text\_change* 21-Jul-2000  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 A:Gene: btp19 *Streptomyces olivaceus* strain 410  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/40/Product: breast-tissue protein btp19 status predicted *CMAT*  
 Query Match 95.4% Score 62; db 2; Length 545;  
 Best Local Similarity 92.3%; Pred. No. 3,0045;  
 Matches 22; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPROSPTLASS 13  
 DB 255 PPROSPTLASS 271

QY 277 PPROSPTLASS 282  
 DB 277 PPROSPTLASS 282

RESULT 5  
 C5511  
 C-peptide - fruit fly (*Drosophila melanogaster*)  
 C:Accession: C5511; Gene: B.M. Waller; January 1995  
 C:Dates: 10-Jun-1998 *sequence\_revision* 10-Jun-1998 *text\_change* 21-Jul-2000  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 A:Gene: btp19 *Streptomyces olivaceus* strain 410  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/40/Product: breast-tissue protein btp19 status predicted *CMAT*  
 Query Match 95.4% Score 62; db 2; Length 403;  
 Best Local Similarity 92.1%; Pred. No. 3,0045;  
 Matches 22; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPROSPTLASS 13  
 DB 260 PPROSPTLASS 272

RESULT 6  
 S51127  
 heparin-binding glycoprotein 18k (btp19) [btp19]  
 C:Accession: S51127; Gene: B.M. Waller; January 1995  
 C:Dates: 19-Mar-1997 *sequence\_revision* 15-Mar-1997 *text\_change* 22-2-2004  
 C:Keywords: submitted to the EMBL Data Library  
 A:Description: Identification of a 33kDa heparin-binding glycoprotein (btp19) in *Dictyostelium*  
 A:Accession: S51127  
 A:Status: Preliminary  
 A:Molecule type: RNA  
 A:Cross-references: EMBL:U081015; KID:q108503; PIRN:CA61603.1; PTD:3614598  
 C:Dates: 10-Jun-1998 *sequence\_revision* 10-Jun-1998 *text\_change* 21-Jul-2000  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 A:Gene: btp19 *Streptomyces olivaceus* strain 410  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/40/Product: breast-tissue protein btp19 status predicted *CMAT*  
 Query Match 91.8%; Score 62; db 2; Length 481;  
 Best Local Similarity 92.3%; Pred. No. 3,0045;  
 Matches 12; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPROSPTLASS 13  
 DB 255 PPROSPTLASS 271

RESULT 7  
 S51127  
 heparin-binding glycoprotein 18k (btp19) [btp19]  
 C:Accession: S51127; Gene: B.M. Waller; January 1995  
 C:Dates: 19-Mar-1997 *sequence\_revision* 15-Mar-1997 *text\_change* 22-2-2004  
 C:Keywords: submitted to the EMBL Data Library  
 A:Description: Identification of a 33kDa heparin-binding glycoprotein (btp19) in *Dictyostelium*  
 A:Accession: S51127  
 A:Status: Preliminary  
 A:Molecule type: RNA  
 A:Cross-references: EMBL:U081015; KID:q108503; PIRN:CA61603.1; PTD:3614598  
 C:Dates: 10-Jun-1998 *sequence\_revision* 10-Jun-1998 *text\_change* 21-Jul-2000  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 C:Keywords: differences at the carboxy end are due to a frameshift error  
 A:Gene: btp19 *Streptomyces olivaceus* strain 410  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/GenBank: local sequence status predicted *ASCO*  
 F1-2/40/Product: breast-tissue protein btp19 status predicted *CMAT*  
 Query Match 95.4% Score 62; db 2; Length 403;  
 Best Local Similarity 92.1%; Pred. No. 3,0045;  
 Matches 22; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PPROSPTLASS 13  
 DB 260 PPROSPTLASS 272



Query Match: 58 5% Score 38, 0u 2: Length 567;  
 Best Local Similarity: 77 8% (Evid. No. 40);  
 Matches: 7: Conservative 1: Mismatches 0: Gaps 0;

QY 1 PFGKSGFTL 9  
 1111111111  
 UO 556 PFGKSGFTL 514

RESULT 13  
 Accession: A9473  
 CDate: 10-Sep-1999 #sequence\_revision: 10-800-1594 \*tax\_change 21-Jul-2002  
 CSpecies: Archaeoglobus fulgidus  
 CDate: 05-Dec-1997 #sequence\_revision: 05-Dec-1997 #tax\_change 18-Aug-2002  
 R.Klein, R.P.: Clayton, R.A.; Tomb, J.P.; White, G.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 J.; Fleischmann, R.D.; Gocayne, J.; Iyer, H.; Sutton, G.G.; Gill, S.; Kinkas, R.P.  
 A. Authors: Artach, T.; Cotton, M.D.; Springs, J.; Artach, P.; Kaine, R.P.; Sykes, S.  
 S.; Smith, N.G.; Woese, C.R.; Wenzel, J.C.  
 AReference number: A94730; NCBI:9806934; PMID:938475  
 AAccession: A9473  
 AReference number: A94730; NCBI:9806934; PMID:938475  
 ATitle: The complete genome sequence of the hyperthermophilic, sulfur-reducing archaeon  
 AResidues: 1-777 \*CDS  
 ANotes: preliminary; nucleic acid sequence not shown; translation not shown  
 ACross-references: GI:4600783; MIM:224502; PIR:MA96211; PIR:Q64875  
 CSuperfamily: Bactillus subsp. B. subtilis 121-131 protein 7475

Query Match: 58 5% Score 37, 0u 2: Length 177;  
 Best Local Similarity: 51 8% (Evid. No. 40);  
 Matches: 7: Conservative 2: Mismatches 0: Gaps 0;  
 QY 2 PFGKSGFTL 2  
 1111111111  
 UO 262 PFGKSGFTL 173

RESULT 14  
 Accession: A9473  
 CDate: 10-Sep-1999 #sequence\_revision: 10-800-1594 \*tax\_change 21-Jul-2002  
 CSpecies: Archaeoglobus fulgidus  
 CDate: 05-Dec-1997 #sequence\_revision: 05-Dec-1997 #tax\_change 18-Aug-2002  
 R.Klein, R.P.: Clayton, R.A.; Tomb, J.P.; White, G.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 J.; Fleischmann, R.D.; Gocayne, J.; Iyer, H.; Sutton, G.G.; Gill, S.; Kinkas, R.P.  
 A. Authors: Artach, T.; Cotton, M.D.; Springs, J.; Artach, P.; Kaine, R.P.; Sykes, S.  
 S.; Smith, N.G.; Woese, C.R.; Wenzel, J.C.  
 AReference number: A94730; NCBI:9806934; PMID:938475  
 ATitle: The complete genome sequence of the hyperthermophilic, sulfur-reducing archaeon  
 AResidues: 1-777 \*CDS  
 ANotes: preliminary; nucleic acid sequence not shown; translation not shown  
 ACross-references: GI:4600783; MIM:224502; PIR:MA96211; PIR:Q64875  
 CSuperfamily: Bactillus subsp. B. subtilis 121-131 protein 7475

Query Match: 58 5% Score 37, 0u 2: Length 205;  
 Best Local Similarity: 60 6% (Evid. No. 40);  
 Matches: 6: Conservative 2: Mismatches 2: Indels 0: Gaps 0;  
 QY 1 PFGKSGFTL 10  
 1111111111  
 UO 342 PFGKSGFTL 151

RESULT 15  
 Accession: A9473  
 CDate: 10-Sep-1999 #sequence\_revision: 10-800-1594 \*tax\_change 21-Jul-2002  
 CSpecies: Archaeoglobus fulgidus  
 CDate: 05-Dec-1997 #sequence\_revision: 05-Dec-1997 #tax\_change 18-Aug-2002  
 R.Klein, R.P.: Clayton, R.A.; Tomb, J.P.; White, G.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 J.; Fleischmann, R.D.; Gocayne, J.; Iyer, H.; Sutton, G.G.; Gill, S.; Kinkas, R.P.  
 A. Authors: Artach, T.; Cotton, M.D.; Springs, J.; Artach, P.; Kaine, R.P.; Sykes, S.  
 S.; Smith, N.G.; Woese, C.R.; Wenzel, J.C.  
 AReference number: A94730; NCBI:9806934; PMID:938475  
 ATitle: The complete genome sequence of the hyperthermophilic, sulfur-reducing archaeon  
 AResidues: 1-777 \*CDS  
 ANotes: preliminary; nucleic acid sequence not shown; translation not shown  
 ACross-references: GI:4600783; MIM:224502; PIR:MA96211; PIR:Q64875  
 CSuperfamily: Bactillus subsp. B. subtilis 121-131 protein 7475

CSpecies: Schizosaccharomyces pombe  
 CDate: 05-Dec-1999 #sequence\_revision: 05-Dec-1999  
 R.Lyne, N.; Bjornstrom, M.A.; Bartell, H.G.; Janda, R.; Gallardo, C.  
 AReference number: 21855  
 AAccession: 139185  
 AReference number: 139185  
 ATitle: The complete genome sequence of the hyperthermophilic, sulfur-reducing archaeon  
 AResidues: 1-610 \*CDS  
 ANotes: preliminary; nucleic acid sequence not shown; translation not shown  
 ACross-references: GI:4600783; MIM:224502; PIR:MA96211; PIR:Q64875  
 CSuperfamily: Bactillus subsp. B. subtilis 121-131 protein 7475

Query Match: 58 5% Score 37, 0u 2: Length 610;  
 Best Local Similarity: 60 6% (Evid. No. 40);  
 Matches: 7: Conservative 2: Mismatches 2: Indels 0: Gaps 0;  
 QY 1 PFGKSGFTL 11  
 1111111111  
 UO 555 PFGKSGFTL 505

Search completed: September 24, 2003, 13:49:13  
 All time: 15:53:38

GenPept version 5.1.6  
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OM protein - protein search, using sw rules

Run on: September 24, 2003, 13:26:37, Search time 4:19:22 S-cons  
Sequence: 65 PTFORSFLASPF 13  
12,738 Million nt. updates/sec

Title: US-09-744-282-5

Perfect score: 65

Scoring table: BLOSUM62

Searched: 127863 seqs, 4726705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 250000050

Post-processing: Maxine Match 0%

Maximum Match 100%

Casting filter 4 summaries

Database: swisprot+st+\*

Pred. No. is the number of results prioritized by chance to have a

score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

Summary:

Result No.	Score	Match	Length	DB ID	Description
1	62	90.4	381	C11L HUMAN	P24222 hemoglobin
2	62	90.4	381	C11L HUMAN	Q11622 hemoglobin
3	62	88.1	390	C102 HUMAN	Q13762 hemoglobin
4	62	88.1	390	C102 HUMAN	Q13762 hemoglobin
5	40	61.5	554	C101 HUMAN	P15362 hemoglobin
6	36	60.0	1159	P411 HUMAN	P92521 hemoglobin
7	36	56.9	1177	P186 HUMAN	Q13412 hemoglobin
8	37	56.9	1177	P186 HUMAN	Q13412 hemoglobin
9	37	56.9	1177	P186 HUMAN	Q13412 hemoglobin
10	37	56.9	1177	P186 HUMAN	Q13412 hemoglobin
11	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
12	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
13	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
14	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
15	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
16	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
17	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
18	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
19	36	55.4	671	C101 HUMAN	Q13412 hemoglobin
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OpenOffice version 5.1.2

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CM proteins - protein regions using an model

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AC A03048:
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XX Human cartilage gp-39 autoimmune peptide #4.
XX human; autoimmune disease; epitope: antigen; rheumatoid arthritis:
XX immunosuppression.
XX Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FI Modified-site 13 /note="connected to C13-(O2G2DIE13-O2H2C2O)"
FI Modified-site 13 /note="C-terminal is amidated"
PN W020012081-A1.
XX 26-APR-2001.
CT 12-OCT-2000; 2000QO-EP10230.
XX 18-OCT-1999; 95SP-020427.
XX (AAKU) AKZO NBEI IV.
PA Van Staveren CJ, Timmers CM, Van Galen EJM, Kneepel RMA, Boes AMH,
P1 Milleburg AMH.
DR WPI 2001-367293/38.
XX Modified peptides derived from human cartilage gp-39 protein epitope
XX are useful in immunotherapy, especially in the treatment of arthritis
XX
XX Claim 12: Page 39; 52pp: English.
XX The sequence represents a modified peptide derived from human cartilage
XX gp-39 protein epitope (amino acids 254-275) for use in immunotherapy.
XX The peptides are useful for inducing tolerance induction in patients
XX suffering from autoimmune diseases such as Rheumatoid arthritis.
XX The peptides provide antigen-specific, non-toxic immunosuppression
XX therapy as a very attractive alternative to non-specific
XX immunosuppression.
XX
XX Sequence 13 AA.
Query Match 100.0%; Score 62; Pos 22; Length 13;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;
CT 12-SEP-2001 (first entry)
XX Human cartilage gp-39 autoimmune peptide #21.
XX human; autoimmune disease; epitope: antigen; rheumatoid arthritis:
XX immunosuppression.
XX Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FI Modified-site 1 /note="C-terminal amide"
FI Modified-site 1 /note="N-terminal"
FI Note-difference 1 /note="N-to-from rna-de"
PN W020012081-A1.

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XX AA020215:
XX 18-JUN-2002 (first entry)
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DE Human cartilage glycoprotein (HC gp)-39 modified peptide #2.
XX
XX major histocompatibility complex, insulin-dependent diabetes mellitus.
XX multiple sclerosis, prostatic, myasthenia gravis, rheumatoid arthritis,
XX rheumatoid arthritis, rheumatoid arthritis, Grave's.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="Linked to HMG2-(C205)-1-(C24)"
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XX AA020214870-A2.
XX
PD 21-FEB-2002.
XX
XX 08-AUG-2002: 100SEP-02059135.
XX
PR 14-AUG-2002: 200SEP-022844.
XX
XX (AAKU) AKZO NOBEL NV.
XX
XX Steenbakkers NV.
XX
DR WP1: 2002-259214/31.
XX
XX Method for diagnosing an autoimmune disease activity by detecting the
XX presence of an autoimmune specific major histocompatibility complex
XX (MHC)-peptide complex in a patient using antibodies specific against
XX MHC-peptide complexes.
XX
XX Example 4: Page 21: 4ppp. English.
XX
XX The patent discloses a method for diagnosing an autoimmune disease
XX activity. The method involves detecting the presence of an autoimmune
XX specific major histocompatibility complex (MHC)-peptide complex in a
XX patient suffering from an autoimmune disease with antibodies or 1S
XX antibodies specific against the MHC-peptide complex. The method
XX peptide. The method and antibodies are useful for diagnosing auto-
XX immune diseases or predicting autoimmune specific MHC-peptide complexes
XX in a patient. The method and antibodies are useful for the manufacture of
XX preparation for the treatment of autoimmune disorders such as insulin-
XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
XX rheumatoid arthritis, rheumatoid arthritis, Grave's.
XX cartilage glycoprotein (HC gp)-39 modified peptide. This peptide is
XX used in the exemplification of the invention.
XX
XX Sequence 13 AA:
XX
XX Query Match 100.0% Score 621 DB 23: Length 13.
XX
XX Best Local Similarity 100.0% P-Val 6e-05:
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XX Matches 13: Conservative 0, Mismatches 0, Indels 0, Gaps 0.
XX
XX 1 RPTASASPTG 13
XX 1 RPTASASPTG 13
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XX Db 1 RPTASASPTG 13
XX 1 RPTASASPTG 13
XX
XX RESULT 14
XX AA020216
XX AA020216 standard: peptide: 13 AA.
XX
XX AC AA020216:
XX
XX 18-JUN-2002 (first entry)
XX
XX Human: cartilage glycoprotein (HC gp)-39 modified peptide #3.

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XX
XX Human: cartilage glycoprotein-39, HC gp-39, autoimmune disorder, MHC,
XX major histocompatibility complex, insulin-dependent diabetes mellitus,
XX multiple sclerosis, prostatic, myasthenia gravis, rheumatoid arthritis,
XX rheumatoid arthritis, rheumatoid arthritis, Grave's.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="N-terminal, cont-1"
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XX X.ac-difference 12
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XX Modified-site 14, 15 /note="This residue is given as Xaa in the sequence
XX as aa 20 in 99, 1 in the sequence listing"
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XX Modified-site 14, 15 /note="linked by pro-oxymer group"
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XX Modified-site 14, 15 /note="N-terminal, cont-2"
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XX WP20214870-A2.
XX
XX 21-FEB-2002.
XX
XX 08-AUG-2002: 200SEP-02059135.
XX
XX 14-AUG-2002: 200SEP-022844.
XX
XX (AAKU) AKZO NOBEL NV.
XX
XX Steenbakkers NV.
XX
XX WP1: 2002-259214/31.
XX
XX Method for diagnosing an autoimmune disease activity by detecting the
XX presence of an autoimmune specific major histocompatibility complex
XX (MHC)-peptide complex in a patient using antibodies specific against
XX MHC-peptide complexes.
XX
XX Example 4: Page 21: 4ppp. English.
XX
XX The patent discloses a method for diagnosing an autoimmune disease
XX activity. The method involves detecting the presence of an autoimmune
XX specific major histocompatibility complex (MHC)-peptide complex in a
XX patient suffering from an autoimmune disease with antibodies or 1S
XX antibodies specific against the MHC-peptide complex. The method
XX peptide. The method and antibodies are useful for diagnosing auto-
XX immune diseases or predicting autoimmune specific MHC-peptide complexes
XX in a patient. The method and antibodies are useful for the manufacture of
XX preparation for the treatment of autoimmune disorders such as insulin-
XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
XX rheumatoid arthritis, rheumatoid arthritis, Grave's.
XX cartilage glycoprotein (HC gp)-39 modified peptide. This peptide is
XX used in the exemplification of the invention.
XX
XX Sequence 13 AA:
XX
XX Query Match 100.0% Score 621 DB 23: Length 13.
XX
XX Best Local Similarity 100.0% P-Val 6e-05:
XX
XX Matches 13: Conservative 0, Mismatches 0, Indels 0, Gaps 0.
XX
XX 1 RPTASASPTG 13
XX 1 RPTASASPTG 13
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XX Db 1 RPTASASPTG 13
XX 1 RPTASASPTG 13
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XX RESULT 15
XX AA020217
XX AA020217 standard: peptide: 13 AA.
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XX AC AA020217:
XX
XX 18-JUN-2002 (first entry)
XX
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1  INFORMATION FOR SEQ ID NO: 2:
2  SEQUENCE CHARACTERISTICS:
3  LENGTH: 15 amino acids
4  STRANDNESS: single
5  TOPOLOGY: linear
6  NAME: 15 amino acids
7  FRAGMENT TYPE: internal
8  US-09-405-745-2
9
10 Query Match
11 Best Local Similarity: 100.0%, Score 62, DB 4, Length 15:
12 Matches 13: Conservative 0, Mismatches 0, Indels 0: Gaps 0:
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14 QY 1 SSTPLASSTG 1
15 DB 3 SSTPLASSTG 15
16
17 RESULT 5
18 US-09-744-705-41
19 Sequence 41: Application US/3917303
20 Patent No. 618124
21 APPLICANT: SCOTTS, ANNA M.H.
22 APPLICANT: VERBIDEN, GILBERTUS F.M.
23 TITLE OF INVENTION: DOPAMINERGIC HYPERK
24 FILE REFERENCE: 0/96-58 US
25 CURRENT FILING DATE: 1997-02-09
26 NUMBER OF SEQ ID NOS: 2
27 SOFTWARE: Patent in Ver. 2.1
28 LENGTH: 15
29 TYPE: PAT
30 FEATURE: Artificial Sequence
31 OTHER INFORMATION: Description of Artificial Sequence: DRIVER PEPT
32 US-09-744-705-41
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34 Query Match
35 Best Local Similarity: 100.0%, Score 27, DB 3, Length 15:
36 Matches 13: Conservative 0, Mismatches 0, Indels 0: Gaps 0:
37
38 QY 2 SSTPLASSTG 13
39 DB 2 SSTPLASSTG 14
40
41 RESULT 6
42 US-09-744-715-3
43 Sequence 3: Application US/940745
44 Patent No. 635020
45 GENERAL INFORMATION:
46 APPLICANT: Abbott Laboratories, Inc.
47 TITLE OF INVENTION: Method of preparing a monoclonal
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: Abbott Laboratories, Inc.
50 STREET: 1360 Pierce Drive, Suite 206
51 CITY: Rockford
52 STATE: Maryland
53 COUNTRY: US
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: floppy disk
56 OPERATING SYSTEM: WINDOWS
57 SOFTWARE: Patent in Release 4.1.0. Version #1.30. (REV)
58 CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER: US/09/405,745
2  FILING DATE:
3  CLASSIFICATION:
4  PRIORITY APPLICATION DATA:
5  APPLICATION NUMBER: US/08/355,898
6  FILING DATE:
7  NAME/AGENT INFORMATION:
8  NAME/AGENT: Scotts, Anna M.H.
9  REGISTRATION NUMBER: 35,477
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: 301-548-9751
12 FAX: 301-548-9751
13 INFORMATION FOR SEQ ID NO: 1:
14 SOURCE: Chemical synthesis
15 LENGTH: 15 amino acids
16 TYPE: amino acid
17 STRANDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: Peptide
20 FRAGMENT TYPE: internal
21 US-09-405-745-3
22
23 Query Match
24 Best Local Similarity: 100.0%, Score 62, DB 4, Length 15:
25 Matches 13: Conservative 0, Mismatches 0, Indels 0: Gaps 0:
26
27 QY 1 SSTPLASSTG 13
28 DB 2 SSTPLASSTG 14
29
30 RESULT 7
31 US-09-450-745-2
32 Sequence 2: Application US/0459740
33 Patent No. 646495
34 GENERAL INFORMATION:
35 APPLICANT: Abbott Laboratories, Inc.
36 TITLE OF INVENTION: Compositions and Methods for Altering Cell Migration
37 FILE REFERENCE: 0794, 219A
38 CURRENT APPLICATION NUMBER: US/09/439,745D
39 PRIORITY APPLICATION NUMBER: 60/111,056
40 PRIORITY FILING DATE: 1998-12-11
41 SOFTWARE: Patent in Ver. 2.1
42 SEQ ID NO 17
43 SOURCE: Chemical synthesis
44 LENGTH: 13
45 TYPE: PAT
46 ORGANISM: Sus scrofa
47 US-09-450-745-2
48
49 Query Match
50 Best Local Similarity: 84.6%, Score 51, DB 4, Length 383:
51 Matches 11: Conservative 0, Mismatches 1, Indels 0: Gaps 0:
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53 QY 1 SSTPLASSTG 13
54 DB 263 SSTPLASSTG 775
55
56 RESULT 8
57 US-08-654-915-2
58 Sequence 4: Application US/0854915
59 Patent No. 685491
60 GENERAL INFORMATION:
61 APPLICANT: Adamou, Julie
62 APPLICANT: Adamou, Robert
63 APPLICANT: Roseberry, Martin
64 TITLE OF INVENTION: HUMAN CARILAGE GP19-LIKE GENE
65 NUMBER OF SEQUENCES:
66 SOURCE: Human cartilage
67 ADDRESSEE: Smithline Beecham Corporation
68 STREET: 705 Swesland Road

```



ADDRESS: ALSO NO. 37505761, BELMONT DEPARTMENT  
 STREET: 1400 PICTARD DRIVE, SUITE 206  
 CITY: ROCKVILLE  
 STATE: MARYLAND  
 COUNTRY: U.S.A.  
 ZIP: 20850  
 COMPUTER: IBM PC COMPATIBLE  
 MEDIUM TYPE: FLOPPY DISK  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA: US/08/619, 645  
 APPLICATION NUMBER: US/08/619, 645  
 CLASSIFICATION: 314  
 ATTORNEY/AGENT INFORMATION:  
 REGISTRATION NUMBER: 31,407  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE NUMBER: 301-946-4311  
 INFORMATION FOR SEQ ID NO. 431  
 SEQUENCE CHARACTERISTICS: 21  
 LENGTH: 9 amino acids  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-619-445-2

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 Matches: 9, Conservative: 9, Mismatches: 0, Gaps: 0

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 GENERAL INFORMATION:  
 APPLICANT: Newman, Roland A.  
 APPLICANT: Rab, Ronald W.  
 TITLE OF INVENTION: Recombinant antibodies for B-cell therapy  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, CONNE, SNECKER & WATERS  
 STREET: 999 PRINCE ST.  
 CITY: ALABAMA  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 23104  
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 FILING DATE: 07 JUN-1995  
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 PUBLICATION DATE:  
 APPLICATION NUMBER: US 08/379, 072  
 FILING DATE: 25 JAN-1995  
 PRIORITY CLAIM: YES  
 APPLICATION NUMBER: US 07/941,292  
 FILING DATE: 10 JUL-1992  
 APPLICATION NUMBER: US 07/895,281  
 FILING DATE: 23 MAR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/735,064  
 FILING DATE: 25 JUL-1991  
 ATTORNEY/AGENT INFORMATION:  
 REGISTRATION NUMBER: 35,610  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE NUMBER: 703-516-2021  
 INFORMATION FOR SEQ ID NO. 69:  
 STRANDNESS: single  
 LENGTH: 25 amino acids  
 MOLECULE TYPE: peptide



TRANSMISSIONS: NOT RELEVANT  
 TOPOLOGY: NO  
 MOLECULE TYPE: PEPTIDE  
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 DB 27 FSLASSTESTNG 37  
 MERRILL 15  
 US-09-439-740-5 Location US/094397405  
 Patent No 646475  
 GENERAL INFORMATION: Albert J. T.  
 TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration  
 FILE REFERENCE: 0794 0154 US/09/450,719/0  
 CURRENT FILING DATE: 1999-12-11  
 PRIOR APPLICATION NUMBER: 65/211,846  
 PRIORITY DATE: 1999-12-11  
 NUMBER OF SEQ ID NOS: 17  
 SEQ-NAME: Patent Invention  
 SEQ-NO 13  
 SEQ-NAME: Patent Invention  
 TYPE: PEPT  
 PROGRAM: Artificial Sequence  
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 OTHER INFORMATION: Peptide corresponding to amino acids 261-273 of  
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 Query Match: Similarity: 67.7%; Reference: 0;  
 Matches: 9; Conservative: 3; Misses: 0; Gaps: 0;  
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 Seq file: 15.7753 seqs

TRANSMISSIONS: NOT RELEVANT  
 TOPOLOGY: NO  
 MOLECULE TYPE: PEPTIDE  
 ORIGINAL SOURCE:   
 POSITION IN GENOME:   
 CHROMOSOME/SEGMENT: V12 clone 2-10  
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 US-09-439-740-5 Location US/094397405  
 Patent No 646475  
 GENERAL INFORMATION: Albert J. T.  
 TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration  
 FILE REFERENCE: 0794 0154 US/09/450,719/0  
 CURRENT FILING DATE: 1999-12-11  
 PRIOR APPLICATION NUMBER: 65/211,846  
 PRIORITY DATE: 1999-12-11  
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 SEQ-NO 13  
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 OTHER INFORMATION: Peptide corresponding to amino acids 261-273 of  
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 DB 3 NESTASSET 12  
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 Seq file: 15.7753 seqs

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OM protein - protein search, amino sw model

Run on: September 24, 2003, 11:47:40, Search time 25 06:21 Seconds

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Title: US-09-744-282-6

Perfect score: 0

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Total number of hits satisfying chosen parameters: 568694

Minimum DB seq length: 0

Maximum DB seq length: 50000000

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Maximum hits: 10

Display first 10 summaries

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Prod. No. is the number of results registered by changes to have 0 score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ATTORNEYS

Sequence 1, Application US/09/94565  
Sequence 2, Application US/09/94565  
Sequence 3, Application US/09/94565  
Sequence 4, Application US/09/94565  
Sequence 5, Application US/09/94565  
Sequence 6, Application US/09/94565  
Sequence 7, Application US/09/94565  
Sequence 8, Application US/09/94565  
Sequence 9, Application US/09/94565  
Sequence 10, Application US/09/94565  
Sequence 11, Application US/09/94565  
Sequence 12, Application US/09/94565  
Sequence 13, Application US/09/94565  
Sequence 14, Application US/09/94565  
Sequence 15, Application US/09/94565  
Sequence 16, Application US/09/94565  
Sequence 17, Application US/09/94565  
Sequence 18, Application US/09/94565  
Sequence 19, Application US/09/94565  
Sequence 20, Application US/09/94565  
Sequence 21, Application US/09/94565  
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Sequence 24, Application US/09/94565  
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Sequence 96, Application US/09/94565  
Sequence 97, Application US/09/94565  
Sequence 98, Application US/09/94565  
Sequence 99, Application US/09/94565  
Sequence 100, Application US/09/94565

1 STRANDNESS: single  
 2 TOPALOGY: linear  
 3 MOLECULE TYPE: protein  
 4 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 5 US-09-985-065-1  
 6  
 7 Query Match 100.0% Score 62.00 Locn 17  
 8 Best Local Similarity 100.0% P-adj No 40-65  
 9 Matches 13: Conservative 0, Mismatches 0, Gaps 0  
 10  
 11 1 RSTLASSTG 13  
 12 DB 1 RSTLASSTG 13  
 13  
 14 RESULT 2  
 15 US-09-985-065-2  
 16 Sequence 2, Application US/985065  
 17 PRIORITY: 1301  
 18 GENERAL INFORMATION:  
 19 APPLICANT: Steenbakkers PCA  
 20 TITLE OF INVENTION: Method of preparing a monoclonal  
 21 NUMBER OF SEQUENCES: 1  
 22 CORRESPONDENCE ADDRESS: US2002141304a, Patent, Mpt.  
 23 STREET: 1300 Piedmont Drive, Suite 255  
 24 CITY: Rockville  
 25 STATE: MD  
 26 COUNTRY: US  
 27 ZIP: 20850  
 28 COMPUTER NAME: PLYM  
 29 MEDIUM TYPE: PLASMID  
 30 COMPUTER: IBM PC compatible  
 31 OPERATING SYSTEM: PC-DOS/MS-DOS  
 32 CURRENT APPLICATION DATA:  
 33 APPLICATION NUMBER: US/09/985-065  
 34 PRIORITY: 1301  
 35 CLASSIFICATION: C01K 26/04, A1C, 2001  
 36 PRIOR APPLICATION DATA:  
 37 APPLICATION NUMBER: US/09/985-065  
 38 FILING DATE: 03-NOV-2001  
 39 ATTORNEY/AGENT INFORMATION:  
 40 NAME: Sullivan, Michael C  
 41 ADDRESS: 1300 Piedmont Drive, Suite 255  
 42 TELECOMMUNICATION INFORMATION:  
 43 TELEPHONE: 301-948-9740  
 44 INFORMATION FOR SEQ ID NO: 2:  
 45 SEQUENCE CHARACTERISTICS:  
 46 LENGTH: 13  
 47 MEDIUM TYPE: PLASMID  
 48 STRANDNESS: single  
 49 MOLECULE TYPE: linear  
 50 FRAGMENT TYPE: Internal  
 51 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 52 US-09-985-065-1  
 53  
 54 Query Match Similarity 100.0% Score 62.00 Locn 17  
 55 Best Local Similarity 100.0% P-adj No 40-65  
 56 Matches 13: Conservative 0, Mismatches 0, Gaps 0  
 57  
 58 1 RSTLASSTG 13  
 59 DB 1 RSTLASSTG 13  
 60  
 61 RESULT 3  
 62 US-09-985-065-3  
 63 Sequence 3, Application US/0998065

1 INDEX NO: US/09/985-065-2  
 2 GENERAL INFORMATION:  
 3 APPLICANT: Steenbakkers PCA  
 4 TITLE OF INVENTION: Method of preparing a monoclonal  
 5 NUMBER OF SEQUENCES: 3  
 6 CORRESPONDENCE ADDRESS: US2002141304a, Patent, Mpt.  
 7 STREET: 1300 Piedmont Drive, Suite 206  
 8 CITY: Rockville  
 9 STATE: MD  
 10 COUNTRY: US  
 11 ZIP: 20850  
 12 COMPUTER NAME: PLYM  
 13 MEDIUM TYPE: PLASMID  
 14 COMPUTER: IBM PC compatible  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 CURRENT APPLICATION DATA:  
 17 APPLICATION NUMBER: US/09/985-065  
 18 PRIORITY: 1301  
 19 CLASSIFICATION: C01K 26/04, A1C, 2001  
 20 PRIOR APPLICATION DATA:  
 21 APPLICATION NUMBER: US/09/985-065  
 22 FILING DATE: 03-NOV-2001  
 23 ATTORNEY/AGENT INFORMATION:  
 24 NAME: Sullivan, Michael C  
 25 ADDRESS: 1300 Piedmont Drive, Suite 206  
 26 TELECOMMUNICATION INFORMATION:  
 27 TELEPHONE: 301-948-9740  
 28 INFORMATION FOR SEQ ID NO: 3:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 13  
 31 MEDIUM TYPE: PLASMID  
 32 STRANDNESS: single  
 33 MOLECULE TYPE: linear  
 34 FRAGMENT TYPE: Internal  
 35 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 36 US-09-985-065-1  
 37  
 38 Query Match Similarity 100.0% Score 62.00 Locn 17  
 39 Best Local Similarity 100.0% P-adj No 40-65  
 40 Matches 13: Conservative 0, Mismatches 0, Gaps 0  
 41  
 42 1 RSTLASSTG 13  
 43 DB 1 RSTLASSTG 13  
 44  
 45 RESULT 4  
 46 US-09-985-065-4  
 47 Sequence 4, Application US/985065  
 48 PRIORITY: 1301  
 49 GENERAL INFORMATION:  
 50 APPLICANT: Steenbakkers PCA  
 51 TITLE OF INVENTION: Method of preparing a monoclonal  
 52 NUMBER OF SEQUENCES: 1  
 53 CORRESPONDENCE ADDRESS: US2002141304a, Patent, Mpt.  
 54 STREET: 1300 Piedmont Drive, Suite 255  
 55 CITY: Rockville  
 56 STATE: MD  
 57 COUNTRY: US  
 58 ZIP: 20850  
 59 COMPUTER NAME: PLYM  
 60 MEDIUM TYPE: PLASMID  
 61 COMPUTER: IBM PC compatible  
 62 OPERATING SYSTEM: PC-DOS/MS-DOS  
 63 CURRENT APPLICATION DATA:  
 64 APPLICATION NUMBER: US/09/985-065  
 65 PRIORITY: 1301  
 66 CLASSIFICATION: C01K 26/04, A1C, 2001  
 67 PRIOR APPLICATION DATA:  
 68 APPLICATION NUMBER: US/09/985-065  
 69 FILING DATE: 03-NOV-2001  
 70 ATTORNEY/AGENT INFORMATION:  
 71 NAME: Sullivan, Michael C  
 72 ADDRESS: 1300 Piedmont Drive, Suite 255  
 73 TELECOMMUNICATION INFORMATION:  
 74 TELEPHONE: 301-948-9740  
 75 INFORMATION FOR SEQ ID NO: 4:  
 76 SEQUENCE CHARACTERISTICS:  
 77 LENGTH: 13  
 78 MEDIUM TYPE: PLASMID  
 79 STRANDNESS: single  
 80 MOLECULE TYPE: linear  
 81 FRAGMENT TYPE: Internal  
 82 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 83 US-09-985-065-1  
 84  
 85 Query Match Similarity 100.0% Score 62.00 Locn 17  
 86 Best Local Similarity 100.0% P-adj No 40-65  
 87 Matches 13: Conservative 0, Mismatches 0, Gaps 0  
 88  
 89 1 RSTLASSTG 13  
 90 DB 1 RSTLASSTG 13  
 91  
 92 RESULT 5  
 93 US-09-985-065-5  
 94 Sequence 5, Application US/985065

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1 SEQ ID NO 56
2 LENGTH: 199
3 TYPE: BPT
4 FEATURE: Artificial Sequence
5 OTHER INFORMATION: Description of Artificial Sequence:0028-Ac single
6 OTHER INFORMATION: Chain recombinant NMC class 11 molecule
US-09-815-837-56
Query Match
Best Local Similarity: 100.0%; Score 62; Db 9; Length 199;
Matches 13: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REFTLASSEQWG 13
DB 6 REFTLASSEQWG 18
RESULT 5
Sequence 60: Application US/09815837
Patent No. US2002008241A1
GENERAL INFORMATION:
APPLICANT: Zhu, Shi-ley
APPLICANT: Zhu, Shi-ley
APPLICANT: Arimilli, Subhashini
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Immune Modulators and Related Methods
CURRENT FILING DATE: 2001-03-22
PRIOR FILING DATE: US 60/191,274
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: US 56/284,403
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 60
LENGTH: 199
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:0028 single
OTHER INFORMATION: Chain recombinant NMC class 11 molecule
US-09-815-837-60
Query Match
Best Local Similarity: 100.0%; Score 63; Db 9; Length 199;
Matches 13: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REFTLASSEQWG 13
DB 6 REFTLASSEQWG 18
RESULT 6
Sequence 102: Application US/09815837
Patent No. US2002008241A1
GENERAL INFORMATION:
APPLICANT: Carter, Harrick
APPLICANT: Zhu, Shi-ley
APPLICANT: Arimilli, Subhashini
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Immune Modulators and Related Methods
CURRENT FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
CURRENT APPLICATION NUMBER: US 60/191,274
US-09-815-837-102
Query Match
Best Local Similarity: 100.0%; Score 62; Db 9; Length 209;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REFTLASSEQWG 13
DB 5 REFTLASSEQWG 17
RESULT 8
Sequence 40: Application US/09815837
Patent No. US2002008241A1
GENERAL INFORMATION:
APPLICANT: Zhu, Shi-ley
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Immune Modulators and Related Methods
CURRENT FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
CURRENT APPLICATION NUMBER: US 60/191,274
US-09-815-837-40

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1 BEFORE FILING DATE: 2000-03-22
2 BEFORE APPLICATION NUMBER: US 60/204,249
3 PRIOR FILING DATE: 2000-03-25
4 PRIOR FILING DATE: 2000-03-25
5 PRIOR FILING DATE: 2000-03-25
6 NUMBER OF SEQ ID NOS: 129
7 SOFTWARE: PatentIn Ver. 2.1
8 LENGTH: 208
9 TYPE: BPT
10 FEATURE: Artificial Sequence
11 OTHER INFORMATION: Description of Artificial
12 Sequence:0028 single
13 OTHER INFORMATION: Chain recombinant NMC class 11 molecule
US-09-815-837-102
Query Match
Best Local Similarity: 100.0%; Score 62; Db 9; Length 208;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REFTLASSEQWG 13
DB 6 REFTLASSEQWG 16
RESULT 7
Sequence 35: Application US/09815837
Patent No. US2002008241A1
GENERAL INFORMATION:
APPLICANT: Carter, Harrick
APPLICANT: Zhu, Shi-ley
APPLICANT: Arimilli, Subhashini
APPLICANT: Wang, Aijun
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Immune Modulators and Related Methods
CURRENT APPLICATION NUMBER: US/09815837
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 209
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:0028 single
OTHER INFORMATION: Chain recombinant NMC class 11 molecule
US-09-815-837-35
Query Match
Best Local Similarity: 100.0%; Score 62; Db 9; Length 209;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REFTLASSEQWG 13
DB 5 REFTLASSEQWG 17
RESULT 8
Sequence 40: Application US/09815837
Patent No. US2002008241A1
GENERAL INFORMATION:
APPLICANT: Zhu, Shi-ley
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Immune Modulators and Related Methods
CURRENT FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
CURRENT APPLICATION NUMBER: US 60/191,274
US-09-815-837-40

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1 APPLICANT: Wang, Aijun  
 2 APPLICANT: Corlia Corporation  
 3 CURRENT APPLICATION NUMBER: US 60/191,274  
 4 FILE REFERENCE: 01408-00567005  
 5 PRIOR FILING DATE: 2000-03-22  
 6 PRIOR APPLICATION NUMBER: US 60/204,249  
 7 PRIOR FILING DATE: 2001-01-23  
 8 PRIOR APPLICATION NUMBER: US 60/264,003  
 9 SOFTWARE: Patent In Ver. 2.1  
 10 SEQ ID NO 45  
 11 TYPE: PRT  
 12 ORGANISM: Artificial Sequence  
 13 OTHER INFORMATION: Description of Artificial Sequence: Chain recombinant MHC class II molecule  
 14 OTHER INFORMATION: Chain recombinant MHC class II molecule  
 15 US-09-815-837-42

Query Match: 100.0%, Score 52, Pos 9, Length 210  
 Best Local Similarity: 100.0%, Pos: No. 4, 00097  
 Matches: 13: Conservative 0; Pseudocodes 0; Indels 0; Gaps 0

QY 1 RSTLASSTGVG 13  
 DB 6 RSTLASSTGVG 18

RESULT: 9  
 US-09-815-837-39  
 1 Sequence 39: Application US/0981837  
 2 FILE REFERENCE: 01408-00567005  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Carter, Derrick  
 5 APPLICANT: Wang, Aijun  
 6 APPLICANT: Corlia Corporation  
 7 CURRENT APPLICATION NUMBER: US 60/191,274  
 8 PRIOR FILING DATE: 2000-03-22  
 9 PRIOR APPLICATION NUMBER: US 60/204,249  
 10 PRIOR FILING DATE: 2001-01-23  
 11 PRIOR APPLICATION NUMBER: US 60/264,003  
 12 SOFTWARE: Patent In Ver. 2.1  
 13 LENGTH: 211  
 14 TYPE: PRT  
 15 ORGANISM: Artificial Sequence  
 16 OTHER INFORMATION: Description of Artificial Sequence: Chain recombinant MHC class II molecule  
 17 OTHER INFORMATION: Chain recombinant MHC class II molecule  
 18 US-09-815-837-39

Query Match: 100.0%, Score 62, Pos 6, Length 211  
 Best Local Similarity: 100.0%, Pos: No. 4, 00097  
 Matches: 13: Conservative 0; Pseudocodes 0; Indels 0; Gaps 0

QY 1 RSTLASSTGVG 13  
 DB 5 RSTLASSTGVG 18

RESULT: 10  
 US-09-815-837-39  
 1 Sequence 39: Application US/0981837  
 2 FILE REFERENCE: 01408-00567005  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Carter, Derrick  
 5 APPLICANT: Wang, Aijun  
 6 APPLICANT: Corlia Corporation  
 7 CURRENT APPLICATION NUMBER: US 60/191,274  
 8 PRIOR FILING DATE: 2000-03-22  
 9 PRIOR APPLICATION NUMBER: US 60/204,249  
 10 PRIOR FILING DATE: 2001-01-23  
 11 PRIOR APPLICATION NUMBER: US 60/264,003  
 12 SOFTWARE: Patent In Ver. 2.1  
 13 LENGTH: 211  
 14 TYPE: PRT  
 15 ORGANISM: Artificial Sequence  
 16 OTHER INFORMATION: Description of Artificial Sequence: Chain recombinant MHC class II molecule  
 17 OTHER INFORMATION: Chain recombinant MHC class II molecule  
 18 US-09-815-837-39

Query Match: 100.0%, Score 62, Pos 6, Length 211  
 Best Local Similarity: 100.0%, Pos: No. 4, 00097  
 Matches: 13: Conservative 0; Pseudocodes 0; Indels 0; Gaps 0

QY 1 RSTLASSTGVG 13  
 DB 6 RSTLASSTGVG 18

RESULT: 11  
 US-09-815-837-37  
 1 Sequence 37: Application US/0981837  
 2 FILE REFERENCE: 01408-00567005  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Carter, Derrick  
 5 APPLICANT: Wang, Aijun  
 6 APPLICANT: Corlia Corporation  
 7 CURRENT APPLICATION NUMBER: US 60/191,274  
 8 PRIOR FILING DATE: 2000-03-22  
 9 PRIOR APPLICATION NUMBER: US 60/204,249  
 10 PRIOR FILING DATE: 2000-03-22  
 11 PRIOR APPLICATION NUMBER: US 60/264,003  
 12 SOFTWARE: Patent In Ver. 2.1  
 13 LENGTH: 212  
 14 TYPE: PRT  
 15 ORGANISM: Artificial Sequence  
 16 OTHER INFORMATION: Description of Artificial Sequence: Chain recombinant MHC class II molecule  
 17 OTHER INFORMATION: Chain recombinant MHC class II molecule  
 18 US-09-815-837-37

Query Match: 100.0%, Score 62, Pos 5, Length 272



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1 PRIOR APPLICATION NUMBER: US 45/266,003
2 PRCR FILING DATE: 2001-01-23
3 NUMBER OF SEQ ID NOS: 125
4 500 Nucleotide Residues
5 500 Nucleotide Residues
6 Length: 213
7 500 Nucleotide Residues
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DB 5 RSFTCLASSFGV 18
Search completed September 24, 2003 14:32:29
Job Time : 25.0874 secs

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us-09-744-282-6.rsp

[illegible]



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PT TRANSDIN 656 665 99 (BY SIMILARITY)
PT TRANSDIN 656 665 100 (BY SIMILARITY)

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Search completed: September 24, 2003, 13:42:48

Job time : 9.17778 sec















[illegible][illegible]

XX	NC12.2.487C-R2.
XX	21 FEB-2002.
XX	06-APR-0021: 2001AC-EM95-26
XX	14 A N 2000; 2000AP-0202544.
XX	ALBU   ARIZO NORBZ. NY.
XX	Nonconformities PCA
XX	REF: 2002.269214/31.

Method for diagnosing an autoimmune disease activity by detecting the presence of an autoantibody to a peptide complex comprising a self-peptide complex in a patient using an enzyme specific anti-self-peptide complexes. *Fluorescence*; Page 43; 4:pp. English.

immune diseases or polypyrrolidone containing peptide compounds. They are also useful in therapy or for the manufacture of pharmaceuticals. The present invention provides a method for the preparation of an insulin preparation for the treatment of autoimmune disorders such as insulin-dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, psoriasis or rheumatoid arthritis. The present sequence is human cartilage glycoprotein (HC gp)-39 peptide (residues 426-338). This peptide is used in the exemplification of the invention.













CC stenosis following vascular trauma or disease and is treat;  
 CC atherogenesis, and anti-sense sequences can be used to treat stenosis, as  
 CC atherogenesis is vital for tumour survival.

50 Sequence 381 AA.

Query Match 80.28, Score 55, ID 21, Length 345;  
 Best Local Similarity 51.78, Pred. No. 0.025;  
 Matches 11: Conservative 1, Mismatches 0, Indels 0, Gaps 0;

0y 1 VQVQSVSKV 12

0b 125 VQVQSVSKV 337

RESULT 14

ID ANM3151

XX ANM3151 standard; pep:Id: 16 AA.

XX ANM3151:

DT 28-APR-1998 (first entry)

XX human cartilage glycoprotein 39 derived peptide 432.

XX Articular cartilage, immunosuppressive therapy; antigen: autologous;

XX human cartilage glycoprotein 39 derived peptide 432.

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XX human cartilage glycoprotein 39 derived peptide 432.

Search completed: September 24, 2003, 15:41:23  
Job time : 53.2711 sec



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RESULT 2
US-08-634-492-7
Sequence 7: Application US/085-44991
GENERAL INFORMATION:
APPLICANT: A.M.E. Boots
APP. CANT: P.S. Bos
TITLE OF INVENTION: No. 38414961 Peptides derived from autoantigen L2-18#
TITLE OF INVENTION: No. 38414961 Peptides derived from autoantigen L2-18#
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Ave. No. 5134961, Postal Department
CITY: Rorvik, 110
STATE: Maryland
ZIP: 20652
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Version 1.1.25
APPLICATION NUMBER: US/08/634-493
FILING DATE: 18-APR-1996
APPLICATION NUMBER: US 08/635,645
FILING DATE: 27-MAR-1996
PRIORITY INFORMATION:
PRIORITY DATE: 29-OCT-1995
PRIORITY NUMBER: PCT/EP95/0420-
PRIORITY NUMBER: 70
PRIORITY NUMBER: No. 94231267
PRIORITY DATE: 27-OCT-1994
PRIORITY APPLICATION DATA: No. 94231267
FILING DATE: 07-APR-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 977-0847
TELEFAX: (313) 977-0847
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: Peptide
US-08-634-492-7
Query Match
Best Local Similarity: 100.0%; Pos. No. 17a-31;
Matches: 13; Conservative 0; Mismatches 0; Gaps 0;
QY - VQDQDSVSKR 13
DE 1 VQDQDSVSKR 13
Sequence 51: Application US/09171705
GENERAL INFORMATION:
APPLICANT: BOOTS, ANN M.H.
APPLICANT: VERHEIJEN, CLARETUS F.M.
TITLE OF INVENTION: IMMUNOSUPPRESSIVE TREATY
FILE REFERENCE: C/94198 US
CURRENT APPLICATION NUMBER: US/09/171,705
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patent in Ver. 2.0

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1 SEQ ID NO 51
2 LENGTH: 16
3 TYPE: Peptide
4 FEATURES: Artificial Sequence
5 OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: DERIVED FROM
6 SEQUENCE INFORMATION: SEQUENCE OF HUMAN CARTILAGE (NC) 157-171.PP
7 US-09-171-705-51
8 Query Match
9 Best Local Similarity: 93.8%; Pos. No. 51; Length: 16;
10 Matches: 12; Conservative 0; Mismatches 0; Gaps 0;
11 QY - VQDQDSVSKR 12
12 DE 1 VQDQDSVSKR 15
13 RESULT 4
14 Sequence 16: Application US/0945974.D
15 Patent No. 6464595
16 GENERAL INFORMATION:
17 APPLICANT: VERHEIJEN, CLARETUS F.M.
18 TITLE OF INVENTION: Compositions and Methods for Altering Cell Migration
19 FILE REFERENCE: 0794,035A
20 CURRENT FILING DATE: 09/08/1996
21 PRIOR APPLICATION NUMBER: 60/111,061
22 SOFTWARE: Patent in Ver. 2.1
23 NUMBER OF SEQ ID NOS: 17
24 SEQ ID NO 16
25 LENGTH: 163
26 TYPE: Peptide
27 US-09-459-740-16
28 Query Match
29 Best Local Similarity: 86.2%; Pos. No. 16; Length: 163;
30 Matches: 11; Conservative 1; Mismatches 0; Gaps 0;
31 QY 1 VQDQDSVSKR 12
32 DE 326 VQDQDSVSKR 137
33 RESULT 5
34 Sequence 5: Application US/09171705
35 Patent No. 6184264
36 GENERAL INFORMATION:
37 APPLICANT: VERHEIJEN, CLARETUS F.M.
38 TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
39 IMMUNOSUPPRESSIVE THERAPY
40 FILE REFERENCE: C/94198 US
41 CURRENT APPLICATION NUMBER: US/09/171,705
42 CURRENT FILING DATE: 1999-02-09
43 SOFTWARE: Patent in Ver. 2.0
44 SEQ ID NO 22
45 LENGTH: 16
46 TYPE: Peptide
47 ORGANISM: Artificial Sequence
48 FEATURES:
49 OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
50 SEQUENCE INFORMATION: SEQUENCE OF HUMAN CARTILAGE (NC) 157-171
51 US-09-171-705-52
52 Query Match
53 Best Local Similarity: 84.4%; Pos. No. 53; Length: 16;
54 Matches: 11; Conservative 0; Mismatches 0; Gaps 0;

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RESULT 9  
US-09-039-198A-14  
1 Sequence 1: 12 Application US/09/039/198A  
2 Best Local Similarity 66.24. Pred. No. 1.5.  
3 Molecule 3; Conservative 4; Nucleic 2; Gaps 0;  
4 GENERAL INFORMATION:  
5 APPLICANT: Gray, Patrick W.  
6 TITLE OF INVENTION: CHITINASE CHITIN BINDING ENZYMES  
7 NUMBER OF SEQUENCES: 34  
8 CORRESPONDENCE ADDRESS: 0'Zole, Gerstle, Murray & Borman  
9 STREET: 233 South Wacker Drive/3500 Sears Tower  
10 CITY: Chicago  
11 STATE: Illinois  
12 COUNTRY: United States of America  
13 ZIP: 60606-6402  
14 COMPUTER: IBM PC compatible  
15 MEDIUM TYPE: Floppy disk  
16 APPLICATION NUMBER: US/09/039/198A  
17 CLASSIFICATION: 435  
18 ATTORNEY/AGENT INFORMATION:  
19 REFERENCE/DOCKET NUMBER: 37866/3495  
20 TELEPHONE: (312) 474-0448  
21 TELEFAX: (312) 474-0448  
22 INFORMATION FOR SEQ ID NO: 14:  
23 LENGTH: 373 amino acids  
24 TYPE: amino acid  
25 TOPOLOGY: linear  
26 MOLECULE TYPE: peptide  
27 US-09-039-198A-14  
28 Query Match  
29 Best Local Similarity 66.24. Pred. No. 1.5.  
30 Molecule 3; Conservative 4; Nucleic 2; Gaps 0;  
31 VOTEDUSVSKV 32  
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1 CLASSIFICATION: 435  
2 ATTORNEY/AGENT INFORMATION:  
3 REFERENCE/DOCKET NUMBER: 37866/3495  
4 TELEPHONE: (312) 474-0448  
5 TELEFAX: (312) 474-0448  
6 INFORMATION FOR SEQ ID NO: 14:  
7 LENGTH: 373 amino acids  
8 TYPE: amino acid  
9 TOPOLOGY: linear  
10 MOLECULE TYPE: peptide  
11 US-09-039-198A-15  
12 Query Match  
13 Best Local Similarity 66.24. Pred. No. 1.5.  
14 Molecule 3; Conservative 4; Nucleic 2; Gaps 0;  
15 VOTEDUSVSKV 13  
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MATCHES 9: CONSERVATIVE 2: MISMATCHES 2: LOCUS 0: GAPS 0:

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DE 311 VYDQDSKRY 323

RESULT 12

US-08-277-559-15  
 Patent No. 67222  
 GENERAL INFORMATION:  
 APPLICANT: Gray, Patrick W.  
 TITLE OF INVENTION: A human culture, its recombinant  
 NUMBER OF SEQUENCES: 17 (human MAF-1 and PC-100)  
 CORRESPONDENCE ADDRESS: C/O Dr. Gerfein, MAF-1 & PC-100  
 STREET: 6400 Santa Monica, 211 Santa Monica Blvd.  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER MAINFRAME FORM: disk  
 OPERATING SYSTEM: IBM PC compatible  
 CURRENT FILING DATE: 09/24/03  
 APPLICATION NUMBER: US/08/277-559  
 CLASSIFICATION: 934  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/463,518  
 ACTION/AGENT INFORMATION:  
 NAME: Han-Lu Chen, JI-Hsueh  
 TELEPHONE: 312/274-6300  
 TELEFAX: 312/274-6300  
 TELEX: 25-3855  
 ADDRESS: 373 amino acids  
 TYPE: single  
 COMPLETENESS: single  
 MOLECULE TYPE: peptide  
 US-08-277-559-15  
 Query Match  
 Best Local Similarity 70.8%; Score 41; DA 4; Length 373;  
 Matches 9: Conservative 2: Mismatches 2: Gaps 0:  
 QY 1 VYDQDSKRY 13  
 DE 311 VYDQDSKRY 323  
 RESULT 13  
 US-08-247-574-14  
 Sequence 14, Application US/08/247-574  
 Patent No. 65957  
 GENERAL INFORMATION:  
 APPLICANT: Gray, Patrick W.  
 TITLE OF INVENTION: A human culture, its recombinant  
 NUMBER OF SEQUENCES: 17 (human MAF-1 and PC-100)  
 CORRESPONDENCE ADDRESS: C/O Dr. Gerfein, MAF-1 & PC-100  
 STREET: 6400 Santa Monica, 211 Santa Monica Blvd.  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER MAINFRAME FORM: disk  
 OPERATING SYSTEM: IBM PC compatible  
 CURRENT FILING DATE: 09/24/03  
 APPLICATION NUMBER: US/08/247-574  
 CLASSIFICATION: 934  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/463,518  
 ACTION/AGENT INFORMATION:  
 NAME: Han-Lu Chen, JI-Hsueh  
 TELEPHONE: 312/274-6300  
 TELEFAX: 312/274-6300  
 TELEX: 25-3855  
 ADDRESS: 373 amino acids  
 TYPE: single  
 COMPLETENESS: single  
 MOLECULE TYPE: peptide  
 US-08-247-574-14  
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 Matches 9: Conservative 2: Mismatches 2: Gaps 0:

1 NUMBER OF SEQ ID NOS: 39  
 2 SOFTWARE: Patent Ver. 2.0  
 3 SEQ ID NO 14  
 4 SEQ ID NO 13  
 5 TYPE: PRT  
 6 ORGANISM: Homo sapiens  
 7 US-08-247-574-14

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 Matches 9: Conservative 2: Mismatches 2: Gaps 0:

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 Sequence 15, Application US/08/247-574  
 Patent No. 65957  
 GENERAL INFORMATION:  
 APPLICANT: Gray, Patrick W.  
 TITLE OF INVENTION: A human culture, its recombinant  
 NUMBER OF SEQUENCES: 17 (human MAF-1 and PC-100)  
 CORRESPONDENCE ADDRESS: C/O Dr. Gerfein, MAF-1 & PC-100  
 STREET: 6400 Santa Monica, 211 Santa Monica Blvd.  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER MAINFRAME FORM: disk  
 OPERATING SYSTEM: IBM PC compatible  
 CURRENT FILING DATE: 09/24/03  
 APPLICATION NUMBER: US/08/247-574  
 CLASSIFICATION: 934  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/463,518  
 ACTION/AGENT INFORMATION:  
 NAME: Han-Lu Chen, JI-Hsueh  
 TELEPHONE: 312/274-6300  
 TELEFAX: 312/274-6300  
 TELEX: 25-3855  
 ADDRESS: 373 amino acids  
 TYPE: single  
 COMPLETENESS: single  
 MOLECULE TYPE: peptide  
 US-08-247-574-15  
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 US-08-442-834-4  
 Sequence 6, Application US/08/442-834  
 Patent No. 65957  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: A human culture, its recombinant  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 STREET: 350 Jericho Turnpike  
 CITY: Jericho  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 11756  
 COMPUTER MAINFRAME FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC/OS/2M/PS  
 CURRENT FILING DATE: 09/24/03  
 APPLICATION NUMBER: US/08/442-834  
 CLASSIFICATION: 934  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/247-574  
 FILING DATE: 09/24/03

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1  ATTORNEY/AGENCY INFORMATION:
2  NAME: BACOT, ROBERT C.
3  REGISTRATION NUMBER: 25, 283
4  REGISTRATION STATE: MISSISSIPPI
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: (515) 822-2550
7  TELEFAX: (515) 822-2550
8  INFORMATION PAR. 822, 2550
9  INFORMATION PAR. 822, 2550
10 SEQUENCE CHARACTERISTICS:
11 Length: 87 nt-no nt-ds
12 Type: unknown
13 STRANDEDNESS: unknown
14 TOPOLOGY: unknown
15 MOTIVATION CODES:
16 HYPOTHESIS: NE
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18 US-08-486-839-A
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20 Query Match: 70.84, Score 46, Jh: 2, Length 87:
21 Best Local Similarity: 59.24, Pred. No. 1.5,
22 Matches: 5: Conservative 2: Radicalness 2, Indels 0, Gaps 0:
23
24 DY: 1: VOTGDQDSVKNRY 13
25
26 DN: 332 VGTGTEVETV 144
27
28 Search completed: September 24, 2003, 13:57:16
29 Job time: 16.7153 mins

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SMCORT version 5.1.6

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OH protein - protein search, using as model:

Run on: September 23, 2003, 15:47:40 : Search time 23.07% Sequences  
(without a : : comments)  
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Title: US-09-744-282-7

Sequence score: 45.0322558567

Sequence: 1

Scoring table: PLUGH622

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Post-processing: Maximum Match 0%

Listing first: 43 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the observed hit. It is printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1

US-09-744-282-7

Sequence 15: Application US/10097340

Publication No. US20030087250A1

GENERAL INFORMATION

APPLICANT: KAREN L. GATT

APPLICANT: KAREN L. GATT

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APPLICANT: KAREN L. GATT

APPLICANT: KAREN L. GATT

APPLICANT: KAREN L. GATT

TITLE OF INVENTION: Nucleic Acid Reagents and Methods for the Identification, Prediction, and Therapy of Ovarian Cancer

FILE REFERENCE: KR-030

CURRENT APPLICATION NUMBER: US/10097340

PRIOR APPLICATION NUMBER: 60/273,025

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

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PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

[illegible]

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1 PRIOR APPLICATION NUMBER: 08 004442.3
2 PRIOR FILING DATE: 2000-02-24
3 PRIOR APPLICATION NUMBER: GB 033005C.4
4 PRIOR FILING DATE: 2000-12-28
5 PRIOR APPLICATION NUMBER: 02/0234.853
6 PRIOR FILING DATE: 2000-12-12
7 NUMBER OF SEQ ID NOS: 308
8 SOFTWARE: FASTA30 FOR Windows Version 4.0
9 SEQ ID NO 1:
10 LENGTH: 14
11 TYPE: PRT
12 TYPED PRT: Homo sapiens
13 US-09-743-385-109
14
15 Query Match 70.8% Score 65; 28 12; Length 14;
16 Best Local Similarity 65.2%, seq. no. 4; 2; Indels 0; Gaps 0;
17 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
18
19 QY 1 VQVQDQSEKVK 10
20 11:11111111
21
22 DB 5 VQVQDQSEKVK 16
23
24 RESULT 6
25 US-10-161-547-11
26 FILE REFERENCE: 2786/35607 US/03/01/61547
27 PUBLICATION NO: US20030102160
28 GENERAL INFORMATION:
29 APPLICANT: Gray, Patrick W.
30 TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
31 TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
32 CURRENT FILING DATE: 2002-05-03
33 PRIOR APPLICATION NUMBER: US/03/01/61547
34 PRIOR FILING DATE: 1999-03-12
35 NUMBER OF SEQ ID NOS: 35
36 SOFTWARE: FASTA30 FOR Windows Version 4.0
37 SEQ ID NO 1:
38 LENGTH: 173
39 TYPE: PRT
40 TYPED PRT: Homo sapiens
41 US-10-161-547-14
42
43 Query Match 70.8% Score 65; 28 12; Length 173;
44 Best Local Similarity 65.2%, seq. no. 4; 2; Indels 0; Gaps 0;
45 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
46
47 QY 1 VQVQDQSEKVK 13
48 11:11111111
49
50 DB 311 VQVQDQSEKVK 323
51
52 RESULT 7
53 US-10-161-547-15
54 FILE REFERENCE: 2786/35607 US/03/01/61547
55 PUBLICATION NO: US20030102160
56 GENERAL INFORMATION:
57 APPLICANT: Gray, Patrick W.
58 TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
59 TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
60 CURRENT FILING DATE: 2002-05-03
61 PRIOR APPLICATION NUMBER: US/03/01/61547
62 PRIOR FILING DATE: 1999-03-12
63 NUMBER OF SEQ ID NOS: 35
64 SOFTWARE: FASTA30 FOR Windows Version 4.0
65 SEQ ID NO 1:
66 LENGTH: 173
67 TYPE: PRT
68 TYPED PRT: Homo sapiens
69 US-10-161-547-16
70
71 Query Match 70.8% Score 65; 28 12; Length 173;
72 Best Local Similarity 65.2%, seq. no. 4; 2; Indels 0; Gaps 0;
73 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
74
75 QY 1 VQVQDQSEKVK 13
76 11:11111111
77
78 DB 411 VQVQDQSEKVK 323
79
80 RESULT 8
81 US-10-161-547-2
82 FILE REFERENCE: 2786/35607 US/03/01/61547
83 PUBLICATION NO: US20030102160
84 GENERAL INFORMATION:
85 APPLICANT: Gray, Patrick W.
86 TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
87 TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
88 CURRENT FILING DATE: 2002-05-03
89 PRIOR APPLICATION NUMBER: US/03/01/61547
90 PRIOR FILING DATE: 1999-03-12
91 NUMBER OF SEQ ID NOS: 35
92 SOFTWARE: FASTA30 FOR Windows Version 4.0
93 SEQ ID NO 2:
94 LENGTH: 466
95 TYPE: PRT
96 TYPED PRT: Homo sapiens
97 US-10-161-547-2
98
99 Query Match 70.8% Score 65; 28 12; Length 466;

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QY - VGYDCSVKSW 13  
- VGYDCSVKSW 13

K. Devan, M.: De Made, M., Madise, A.C.; Givax, L.A.; Hencioff, I.: Kees, H.M.N.

Submitting to the protocol database



A: Reference number: 215483

A: Accession: Q12757

A: Species: *Caenorhabditis elegans*

A: Residues: 178 Amino Acids

A: CDSs-References: EMBL:AL324486

A: Experimental source: Cultivar: Columbia; PAC clone T145

A: Map position: 4

A: Ions: 231V

A: MS/MS: 110

C: Superfamily: Strappedous chitinase chi10

Query Match: 54.6%; Score 32; 20; 2; Length 395

Best Local Similarity: 53.6%;

Match: 7; Conservative 3; Indels 0;

Matches 1; VOTDQDSVSKV 13

Db 321 IYDMDSDIVSKV 33;

RESULT 13

C: Species: *Caenorhabditis elegans*

C: Species: *Caenorhabditis elegans*

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GenCode version: 5.1.6

Copyright (c) 1999 - 2003 Computo Ltd.

OM protein - protein search, using BLAST model

Run on: September 24, 2003, 15:42:37, search time 8.1976 seconds

(without alignments)

34,739 million raw updates/sec

Title: US-09-744-282-7

Sort key score: 65

Sequence: 1 V3VDQWQWVKV 23

Scoring table: H3C5062

Gap: 10.0, Gapext: 0.5

Searched: 127863 seqs, 4702673 residues

Total number of hits satisfying chosen parameters: 11865

Maximum DB seq length: 11865

Maximum DB seq length: 2000-2000

Post-processing: Minimum match: 40

Minimum match: 40

Lasting first 40 residues

Database: SWISSPROT 41.4

Pred No. is the number of results predicted by cluster to have a

score greater than or equal to the score of the result being printed.

and is derived by analysis of the local score matrix.

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34	35	53	8	530	1	JPEN-DHMA
35	35	53	8	1553	1	TPSA-CHTFK
36	35	53	8	4952	1	DRC-TPAS
37	35	53	8	2771	1	KNS9-FAHO
38	52	52	3	2771	1	KNS9-FAHO
39	34	52	3	310	1	ARAC-EPHCH
40	34	52	3	339	1	ARAC-EPHCH
41	34	52	3	339	1	ARAC-EPHCH
42	54	52	3	335	1	ARAC-EPHCH
43	34	52	3	362	1	ARAC-EPHCH
44	34	52	3	362	1	ARAC-EPHCH
45	34	52	3	441	1	KNS9-EPHCH

ALIGNMENTS

RESULT 1

RESULT 1

34 35 53 8 530 1

35 35 53 8 1553 1

36 35 53 8 4952 1

37 35 53 8 2771 1

38 52 52 3 2771 1

39 34 52 3 310 1

40 34 52 3 339 1

41 34 52 3 339 1

42 54 52 3 335 1

43 34 52 3 362 1

44 34 52 3 362 1

45 34 52 3 441 1

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## ALIGNMENTS

RESULT 1	34	52	3	310	1	ARAC-EPHCH	P07612 epinis chr
RESULT 1	34	52	3	339	1	ARAC-EPHCH	P07612 epinis chr
RESULT 1	34	52	3	335	1	ARAC-EPHCH	P27005 xenopus lse
RESULT 1	34	52	3	362	1	ARAC-EPHCH	P27005 xenopus lse
RESULT 1	34	52	3	441	1	KNS9-FAHO	P56089 thermoga
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
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RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
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RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
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RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
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RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
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RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34	52	3	4952	1	DRC-TPAS	P35022 saccharomy
RESULT 1	34						

[illegible]













[illegible][illegible]





































RESULT 9  
 US-07-603-636A-2  
 1 Sequence 2, Application US/07064636A  
 2 GENERAL INFORMATION:  
 3 APPLICANT: NORTIDE, TRAVIS C., TERRY E., MELMARIA, LANCE E., PERMYAK,  
 4 TITLE OF INVENTION: IMMUNIZATION AGAINST BACTERIALS USING  
 5 TITLE OF INVENTION: PURIFIED SURFACE ANTIGENS OF BARNSEA HIGEMINA AND KILLAR  
 6 NUMBER OF SEQUENCES: 1  
 7 NUMBER OF SEQUENCES: 1  
 8 CORRESPONDENCE ADDRESS:  
 9 ADDRESSEE: DAVID R. SALAMANCHIN  
 10 ADDRESS: 34200 N. GAINESVILLE, SUITE A-1  
 11 CITY: GAINESVILLE  
 12 STATE: FLORIDA  
 13 ZIP: 32606  
 14 COMPUTER READABLE FORM:  
 15 OPERATING SYSTEM: IBM PC compatible  
 16 OPERATING SYSTEM: PC-DOS/MS-DOS  
 17 CURRENT APPLICATION DATA: 1.0, Version 1.2  
 18 APPLICATION NUMBER: US/074636A  
 19 FILING DATE: 1991-12-22  
 20 FILING DATE: 1991-12-22  
 21 ATTORNEY/AGENT INFORMATION:  
 22 NAME: SALAMANCHIN, DAVID R.  
 23 REFERENCE/COCKET NUMBER: 984 059 71  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEFAX: 924-372-5800  
 26 INFORMATION FOR SEQ ID NO: 2:  
 27 SOURCE CHARACTERISTICS:  
 28 TYPE: AMINO ACID  
 29 MOLECULE TYPE: protein  
 30 US-07-603-636A-2

Query Match 51.0%, Score 316, ID 1, Length 457,  
 Best Local Similarity 24.5%, Prod. No. 74402, 1, 1, data 0, Date 0  
 Matches 6, Conservative 4, Mismatches 1, 1, data 0, Date 0

CY 1 SEQRESKASNT 11  
 DB 265 ASSEKASNT 275

RESULT 11 705 13  
 1 Sequence 13, Application US/931775  
 2 Patent No. 6,64204  
 3 APPLICANT: JUDGE, ANNA W.B.  
 4 APPLICANT: VERHEIJER, GILBERTUS F. M.  
 5 TITLE OF INVENTION: NOVEL PEPTIDES BL-RLNP PEP USE IN ANTI-ONCOGENIC  
 6 FILE REFERENCE: 0/56198 US  
 7 CURRENT APPLICATION NUMBER: 05/99/171,705  
 8 NUMBER OF SEQ ID NOS: 75  
 9 SOFTWARE: PNAS-Inf Ver. 2.0  
 10 LENGTH: 18  
 11 TYPE: PPT  
 12 FEATURE: Artificial Sequence  
 13 OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM  
 14 OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (H2) -39 PROTEIN  
 15 US-05-931775-13

Query Match 50.0%, Score 33, ID 3, Length 15,  
 Best Local Similarity 100.0%, Prod. No. 6,7,  
 Matches 7, Conservative 0, Mismatches 0, Gaps 0,  
 CY 1 SEQRESK 7  
 DB 10 SEQRESK 16

RESULT 11  
 1 Sequence 32, Application US/0807499  
 2 GENERAL INFORMATION:  
 3 APPLICANT: MOYER, Richard N.  
 4 APPLICANT: GILLES, E. P.  
 5 TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a  
 6 NUMBER OF SEQUENCES: Live Vaccines Vector  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: David R. Salamanchin  
 9 ADDRESS: 34200 N. GAINESVILLE, SUITE A-1  
 10 CITY: Gainesville  
 11 STATE: Florida  
 12 ZIP: 32606  
 13 COMPUTER READABLE FORM:  
 14 OPERATING SYSTEM: IBM PC compatible  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 CURRENT APPLICATION DATA: Release #1.0, Version: #1.25  
 17 APPLICATION NUMBER: US/08/07499

FILING DATE: 1995-07-15  
 FILING DATE: 1995-07-15  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/498,241  
 PUBLICATION NUMBER: US 5,740,192  
 PUBLICATION DATE: 1998-07-15  
 APPLICATION NUMBER: US 07/938,630  
 PUBLICATION DATE: 1992-07-15  
 CLASSIFICATION: 435  
 CLASSIFICATION: 435  
 PUBLICATION DATE: 1992-07-15  
 PUBLICATION DATE: 1992-07-15  
 CLASSIFICATION: 435  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 REGISTRATION NUMBER: 31,754  
 REFERENCE/COCKET NUMBER: US/95,1 FWO11  
 TELEFAX: 904-372-5800  
 TELEFAX: 904-372-5800  
 SEQUENCE CHARACTERISTICS:  
 TYPE: amino acid  
 MOLECULE TYPE: protein

US-08-0807499-32  
 Query Match 50.0%, Score 33, ID 3, Length 140,  
 Best Local Similarity 54.3%, Prod. No. 1,80-02,  
 Matches 6, Conservative 3, Mismatches 2, 1, data 0, Gaps 0,  
 CY 1 SEQRESKASNT 11  
 DB 147 SEQRESK 157

RESULT 12

us-09-744-282-8.rai

Wed Sep 24 15:53:56 2003

1 CURRENT APPLICATION NUMBER: US/03/294,924A  
2 PRIOR FILING DATE: 1998-11-23  
3 SEQ NO 2325  
4 APP NO 655795  
5 LENGTH: 340  
6 TYPE: PRT  
7 ORGANISM: *Chlamydia pneumoniae*  
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US-09-295-268-12

1 : Sequence 32, Application: US/0929268

2 : Patent No. 6,275,929

3 : APPLICANT: Novak, Richard W.

4 : APPLICANT: vi uca, Radio

5 : TITLE OF INVENTION: Use of penicillanic acide formate as a

6 : TITLE OF INVENTION: flavo bacillus

7 : NUMBER OF SEQUENCES: 60

8 : ADDRESS: David P. St. James

9 : STREET: 2421 N.W. 44th Street, Miami A-1

10 : CITY: Miami, Fla

11 : STATE: Florida

12 : COUNTRY: U.S.A.

13 : ZIP: 33005

14 : COMPLETION DATE FORM:

15 : INSDIM TYPE: floppy disk

16 : COMPUTER: IBM PC compatible

17 : SOFTWARE: IBM PC compatible

18 : SOFTWARE: IBM PC compatible

19 : CURRENT APPLICATION DATA: US-92/068, 24;

20 : APPLICATION NUMBER: US/09/297,268

21 : CLASSIFICATION:

22 : PRIOR APPLICATION DATA:

23 : APPLICATION NUMBER: US/91/1,127

24 : FILING DATE: 27-APR-1992

25 : APPLICATION NUMBER: US 07/959,241

26 : FILING DATE: 17-JUN-1992

27 : APPLICATION NUMBER: US 07/968,630

28 : FILING DATE: 29-JUN-1992

29 : PRIOR APPLICATION DATA:

30 : APPLICATION NUMBER: US 07/344,212

31 : FILING DATE: 21-APR-1992

32 : ATTORNEY/AGENCY INFORMATION:

33 : NAME: Salomonson, David R

34 : TELECOMMUNICATION INFORMATION:

35 : REFERENCE/DOCKET NUMBER: JET-1, FAKU-1

36 : TELEPHONE: 664-375,890

37 : INFORMATION FOR SEQ. IN NO. 32:

38 : SEQUENCE CHARACTERISTICS:

39 : TYPE: amino acid

40 : TOPOLOGY: Linear

41 : ANALYSIS TYPE: protein

42 : US-09-295-268-12

43 : Query Match

44 : Similarity

45 : Comparison

46 : MATCHES

47 : 50.04

48 : 33

49 : 3

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US-09-232-991A-23129

Query Match: 50.0% Score 33: DN 4: Length 632:  
Best Local Similarity: 100.0% Ref 2:  
Matches: 0: Conserved: 4: Mismatches: 4: Gaps: 0:

07 1 SOWSKIANFQSK 14  
CB 376 SSWFSFAARQK 389

Search completed: September 24, 2003, 13:51:17  
Job time: 17.9888 secs





1 CURRENT APPLICATION NUMBER: 38/10/124,692  
 2 PRIOR FILING DATE: 2002-03-27  
 3 PRIOR APPLICATION NUMBER: US 2002/004,614  
 4 PRIOR FILING DATE: 2002-06-28  
 5 PRIOR APPLICATION NUMBER: US 62/157,137  
 6 PRIOR FILING DATE: 2002-06-28  
 7 PRIOR APPLICATION NUMBER: US 60/113,260  
 8 PRIOR FILING DATE: 1999-11-23  
 9 SOFTWARE: Patent Invention 3.0  
 10 SEQ ID NO 5185  
 11 LENGTH: 8  
 12 ORGANISM: Homo sapiens  
 13 US-09-104-698-5185  
 14  
 15 Query Watch  
 16 Best Local Similarity: 51.58, Prod No: 22,  
 17 Matches: 8, Conservative: 2, Mismatch: 4, Indels: 0, Gaps: 0  
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 19 Qy 1 SWFKSLKQSN 14  
 20 DB 21 ACNRSNATQSN 34  
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1 CURRENT APPLICATION NUMBER: US 08/413,477  
 2 PRIOR FILING DATE: 1997-04-01  
 3 PRIOR APPLICATION NUMBER: US 62/157,137  
 4 PRIOR FILING DATE: 2002-06-28  
 5 PRIOR APPLICATION NUMBER: US 60/113,260  
 6 PRIOR FILING DATE: 1999-11-23  
 7 SOFTWARE: Patent Invention 3.0  
 8 SEQ ID NO 5190  
 9 LENGTH: 8  
 10 ORGANISM: Helicobacter pylori  
 11 US-09-881-7524-5190  
 12  
 13 Query Watch  
 14 Best Local Similarity: 51.58, Prod No: 22,  
 15 Matches: 8, Conservative: 2, Mismatch: 4, Indels: 0, Gaps: 0  
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 17 Qy 1 SWFKSLKQSN 13  
 18 DB 136 SOUTHERNBLAST 148  
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Query Match: 51 5A: Score 34; Dn 10; Length 157;  
 Best Local Similarity: 63 5A: Pos 60; L 20-15;  
 Matches 7: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SEQKASCTSG 14  
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Db 24% AGRKSLTENT 1484

RESULT 14  
 1 Sequence 16: Application US/0902157  
 2 Patent No US2002014607A1  
 3 INVENTOR:  
 4 APPLICANT:  
 5 TITLE OF INVENTION: RNA specific antisense and peptides  
 6 TITLE OF INVENTION: of the Weizmann Institute in the field of antisense and peptides  
 7 NUMBER OF SEQUENCES: 95  
 8 NUMBER OF SEQUENCES: 95  
 9 COMPUTER READABLE FORM:  
 10 COMPUTER READABLE FORM:  
 11 COMPUTER READABLE FORM:  
 12 OPERATING SYSTEM: PC/MS-DOS  
 13 CURRENT APPLICATION DATE: 05/09/2000  
 14 APPLICATION NUMBER: 05/09/2000  
 15 PRIOR APPLICATION DATE: 05/09/2000  
 16 APPLICATION NUMBER: 05/09/2000  
 17 FILING DATE: 05/09/2000  
 18 INVENTOR: 05/09/2000  
 19 LENGTH: 1581 nucleotides  
 20 STRANDEDNESS: single  
 21 TOPOLOGY: linear  
 22 NUCLEIC ACID TYPE: polynucleotide  
 23 NAME/REV: Peptide  
 24 LOCATION: 1-1591  
 25 US-09-428-477-38

Query Match Similarity: 51 5A: Score 34; Dn 10; Length 157;  
 Best Local Similarity: 63 5A: Pos 60; L 20-15;  
 Matches 7: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SEQKASCTSG 14  
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Db 808 RYSJQJLTLR 919

RESULT 15  
 1 US-10-366-511-1  
 2 PUBLICATION NO: US2003055071A1  
 3 INVENTOR: M. K.  
 4 APPLICANT: Genzyme, Inc.  
 5 APPLICANT: Genzyme, Inc.  
 6 APPLICANT: Genzyme, Inc.  
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 25 APPLICANT: Genzyme, Inc.

Query Match Similarity: 51 5A: Score 34; Dn 10; Length 157;  
 Best Local Similarity: 63 5A: Pos 60; L 20-15;  
 Matches 7: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SEQKASCTSG 14  
 1111111111

Db 808 RYSJQJLTLR 919

RESULT 15  
 1 US-10-366-511-1  
 2 PUBLICATION NO: US2003055071A1  
 3 INVENTOR: M. K.  
 4 APPLICANT: Genzyme, Inc.  
 5 APPLICANT: Genzyme, Inc.  
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 25 APPLICANT: Genzyme, Inc.

Query Match Similarity: 51 5A: Score 34; Dn 10; Length 157;  
 Best Local Similarity: 63 5A: Pos 60; L 20-15;  
 Matches 7: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SEQKASCTSG 14  
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Db 808 RYSJQJLTLR 919

RESULT 15  
 1 US-10-366-511-1  
 2 PUBLICATION NO: US2003055071A1  
 3 INVENTOR: M. K.  
 4 APPLICANT: Genzyme, Inc.  
 5 APPLICANT: Genzyme, Inc.  
 6 APPLICANT: Genzyme, Inc.  
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 23 APPLICANT: Genzyme, Inc.  
 24 APPLICANT: Genzyme, Inc.  
 25 APPLICANT: Genzyme, Inc.

Query Match Similarity: 51 5A: Score 34; Dn 10; Length 157;  
 Best Local Similarity: 63 5A: Pos 60; L 20-15;  
 Matches 7: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SEQKASCTSG 14  
 1111111111

Db 808 RYSJQJLTLR 919

RESULT 15  
 1 US-10-366-511-1  
 2 PUBLICATION NO: US2003055071A1  
 3 INVENTOR: M. K.  
 4 APPLICANT: Genzyme, Inc.  
 5 APPLICANT: Genzyme, Inc.  
 6 APPLICANT: Genzyme, Inc.  
 7 APPLICANT: Genzyme, Inc.  
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 22 APPLICANT: Genzyme, Inc.  
 23 APPLICANT: Genzyme, Inc.  
 24 APPLICANT: Genzyme, Inc.  
 25 APPLICANT: Genzyme, Inc.

Seq 75 No 1  
 Length: 2015  
 Type: PRT  
 Genbank  
 55-10-246-2011

Query Match: 51 5A: Score 34; Dn 10; Length 2015;  
 Best Local Similarity: 63 5A: Pos 60; L 20-15;  
 Matches 7: Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 SEQKASCTSG 14  
 1111111111

Db 808 RYSJQJLTLR 919

Search completed September 24, 2003, 14:21:31.  
 CPU time: 32.3034 secs









No.	Result	Query	Score	Match	Length	DB	Description
1	46	100.0	332			GI11_WKSN	P08122
2	46	69.7	332			GI11_WKSN	P08122
3	39	59.1	124			ALAN_SPAH	O08345
4	39	59.1	124			ALAN_SPAH	O08345
5	40	58.3	420			HLIK_LBPA	P17446
6	36	54.5	554			MD12_EAST	P17446
7	36	54.5	554			MD12_EAST	P17446
8	36	54.5	554			MD12_EAST	P17446
9	35	53.0	370			SP12_EAST	P13111
10	35	53.0	613			SP12_EAST	P13111
11	35	53.0	613			SP12_EAST	P13111
12	34	51.4	415			SE14_WKSN	P08122
13	34	51.4	415			SE14_WKSN	P08122
14	34	51.4	415			SE14_WKSN	P08122
15	34	51.4	415			SE14_WKSN	P08122
16	34	51.4	415			SE14_WKSN	P08122
17	34	51.4	415			SE14_WKSN	P08122
18	34	51.4	415			SE14_WKSN	P08122
19	34	51.4	415			SE14_WKSN	P08122
20	33	50.0	261			DR12_EAST	P13111
21	33	50.0	261			DR12_EAST	P13111
22	33	50.0	261			DR12_EAST	P13111
23	33	50.0	261			DR12_EAST	P13111
24	33	50.0	261			DR12_EAST	P13111
25	33	50.0	261			DR12_EAST	P13111
26	33	50.0	261			DR12_EAST	P13111
27	33	50.0	261			DR12_EAST	P13111
28	33	50.0	261			DR12_EAST	P13111
29	33	50.0	261			DR12_EAST	P13111
30	33	50.0	261			DR12_EAST	P13111
31	33	50.0	261			DR12_EAST	P13111
32	33	50.0	261			DR12_EAST	P13111
33	33	50.0	261			DR12_EAST	P13111
34	33	50.0	261			DR12_EAST	P13111
35	33	50.0	261			DR12_EAST	P13111
36	33	50.0	261			DR12_EAST	P13111
37	33	50.0	261			DR12_EAST	P13111
38	33	50.0	261			DR12_EAST	P13111
39	33	50.0	261			DR12_EAST	P13111
40	33	50.0	261			DR12_EAST	P13111
41	33	50.0	261			DR12_EAST	P13111
42	33	50.0	261			DR12_EAST	P13111
43	33	50.0	261			DR12_EAST	P13111
44	33	50.0	261			DR12_EAST	P13111
45	33	50.0	261			DR12_EAST	P13111
46	33	50.0	261			DR12_EAST	P13111
47	33	50.0	261			DR12_EAST	P13111
48	33	50.0	261			DR12_EAST	P13111
49	33	50.0	261			DR12_EAST	P13111
50	33	50.0	261			DR12_EAST	P13111
51	33	50.0	261			DR12_EAST	P13111
52	33	50.0	261			DR12_EAST	P13111
53	33	50.0	261			DR12_EAST	P13111
54	33	50.0	261			DR12_EAST	P13111
55	33	50.0	261			DR12_EAST	P13111
56	33	50.0	261			DR12_EAST	P13111
57	33	50.0	261			DR12_EAST	P13111
58	33	50.0	261			DR12_EAST	P13111
59	33	50.0	261			DR12_EAST	P13111
60	33	50.0	261			DR12_EAST	P13111
61	33	50.0	261			DR12_EAST	P13111
62	33	50.0	261			DR12_EAST	P13111
63	33	50.0	261			DR12_EAST	P13111

- (uq, qis)

[illegible]

















Query Match 51.5% Score 35; DB 1; Length 705;  
Best Local Similarity 50.0%; Pred. No. 8;  
Matches 7; Conservative 2; Miscellaneous 5; Indels 0; Gaps 0;  
QY 1 SORPKIASTQSP 14  
LE 446 SGNRLKQTHNR 5/5

Search completed: September 24, 2003, 15:42:36  
Job time: 5,806.56 sec

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 24, 2003, 13:33:45

Title: US-09-744-282-8  
Percent score: 46  
Sequence: 1-368/368 (100.0%)  
Scoring table: 1-368/368 (100.0%)  
Search: 1-368/368 (100.0%)  
Total number of hits satisfying chosen parameters: 23525

Minimum DB seq length: 500/500/500

Maximum DB seq length: 200/200/200

Post-processing: Minimal Matrix 0%

Clustering: 15 summaries

Database: 1-368/368 (100.0%)

1- SP-368/368 (100.0%)

2- SP-368/368 (100.0%)

3- SP-368/368 (100.0%)

4- SP-368/368 (100.0%)

5- SP-368/368 (100.0%)

6- SP-368/368 (100.0%)

7- SP-368/368 (100.0%)

8- SP-368/368 (100.0%)

9- SP-368/368 (100.0%)

10- SP-368/368 (100.0%)

11- SP-368/368 (100.0%)

12- SP-368/368 (100.0%)

13- SP-368/368 (100.0%)

14- SP-368/368 (100.0%)

15- SP-368/368 (100.0%)

16- SP-368/368 (100.0%)

17- SP-368/368 (100.0%)

18- SP-368/368 (100.0%)

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27- SP-368/368 (100.0%)

28- SP-368/368 (100.0%)

29- SP-368/368 (100.0%)

30- SP-368/368 (100.0%)

31- SP-368/368 (100.0%)

32- SP-368/368 (100.0%)

33- SP-368/368 (100.0%)

Result	No.	Score	Query	Length	DB ID	Description
1	65	100.0	368	4	09617	09617 Homo sapien
2	55	100.0	368	4	09144	09144 Homo sapien
3	46	96.9	368	4	09617	09617 Homo sapien
4	46	96.9	368	4	09144	09144 Homo sapien
5	46	96.9	368	4	09617	09617 Homo sapien
6	46	96.9	368	4	09144	09144 Homo sapien
7	46	96.9	368	4	09617	09617 Homo sapien
8	46	96.9	368	4	09144	09144 Homo sapien
9	46	96.9	368	4	09617	09617 Homo sapien
10	46	96.9	368	4	09144	09144 Homo sapien
11	46	96.9	368	4	09617	09617 Homo sapien
12	39	59.1	705	8	03172	03172 Homo sapien
13	39	59.1	705	8	03172	03172 Homo sapien
14	39	59.1	705	8	03172	03172 Homo sapien
15	39	59.1	705	8	03172	03172 Homo sapien
16	39	59.1	705	8	03172	03172 Homo sapien

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Length	DB ID	Description
1	65	100.0	368	4	09617	09617 Homo sapien
2	55	100.0	368	4	09144	09144 Homo sapien
3	46	96.9	368	4	09617	09617 Homo sapien
4	46	96.9	368	4	09144	09144 Homo sapien
5	46	96.9	368	4	09617	09617 Homo sapien
6	46	96.9	368	4	09144	09144 Homo sapien
7	46	96.9	368	4	09617	09617 Homo sapien
8	46	96.9	368	4	09144	09144 Homo sapien
9	46	96.9	368	4	09617	09617 Homo sapien
10	46	96.9	368	4	09144	09144 Homo sapien
11	46	96.9	368	4	09617	09617 Homo sapien
12	39	59.1	705	8	03172	03172 Homo sapien
13	39	59.1	705	8	03172	03172 Homo sapien
14	39	59.1	705	8	03172	03172 Homo sapien
15	39	59.1	705	8	03172	03172 Homo sapien
16	39	59.1	705	8	03172	03172 Homo sapien

## MISCELLANEOUS

Result	No.	Score	Query	Length	DB ID	Description
1	65	100.0	368	4	09617	09617 Homo sapien
2	55	100.0	368	4	09144	09144 Homo sapien
3	46	96.9	368	4	09617	09617 Homo sapien
4	46	96.9	368	4	09144	09144 Homo sapien
5	46	96.9	368	4	09617	09617 Homo sapien
6	46	96.9	368	4	09144	09144 Homo sapien
7	46	96.9	368	4	09617	09617 Homo sapien
8	46	96.9	368	4	09144	09144 Homo sapien
9	46	96.9	368	4	09617	09617 Homo sapien
10	46	96.9	368	4	09144	09144 Homo sapien
11	46	96.9	368	4	09617	09617 Homo sapien
12	39	59.1	705	8	03172	03172 Homo sapien
13	39	59.1	705	8	03172	03172 Homo sapien
14	39	59.1	705	8	03172	03172 Homo sapien
15	39	59.1	705	8	03172	03172 Homo sapien
16	39	59.1	705	8	03172	03172 Homo sapien

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5	46	96.9	368	4	09617	09617 Homo sapien
6	46	96.9	368	4	09144	09144 Homo sapien
7	46	96.9	368	4	09617	09617 Homo sapien
8	46	96.9	368	4	09144	09144 Homo sapien
9	46	96.9	368	4	09617	09617 Homo sapien
10	46	96.9	368	4	09144	09144 Homo sapien
11	46	96.9	368	4	09617	09617 Homo sapien
12	39	59.1	705	8	03172	03172 Homo sapien
13	39	59.1	705	8	03172	03172 Homo sapien
14	39	59.1	705	8	03172	03172 Homo sapien
15	39	59.1	705	8	03172	03172 Homo sapien
16	39	59.1	705	8	03172	03172 Homo sapien









